

SEQUENCE LISTING

<110> Genencor International, Inc.  
 The Proctor & Gamble Company  
 Jones, Brian E.  
 Kolkman, Marc  
 Leeflang, Chris  
 Oh, Hiroshi  
 Poulose, A.J.  
 Sadlowski, Eugene S.  
 Shaw, Andrew  
 van der Kleij, Wilhelmus A.H.  
 van Marrenwijk, Leo

<120> Serine Proteases, Nucleic Acids Encoding Serine Enzymes and Vectors and Host Cells Incorporating Same

<130> GC819-2-US/B

<140> 10/576,331

<141> 2006-04-18

<150> US 60/523,609

<151> 2003-11-19

<160> 656

<170> PatentIn version 3.2

<210> 1

<211> 1680

<212> DNA

<213> Cellulomonas strain 69B4

<400> 1

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<212> DNA  
<213> Cellulomonas strain 69B4

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<210> 3  
<211> 1404  
<212> DNA  
<213> Cellulomonas spp.

<400> 3

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gacgcgtcg	aggaggtcga	gggcgaaggc	gccacggccg	tcaccgtcg	gcactccctg	300
gccgacccctg	aggcctggaa	gaccgtcctc	gacgcgc	tcgagggcga	cgacgcgtg	360
cccacctgggt	acgtcgacgt	cccgaccaac	agcgtcg	tcgcccgtcaa	ggccggagcc	420
caggacgtcg	ccgcccggct	cgtcgaaagg	gccgacgtcc	cgtccgacgc	cgtgaccc	480
gtcgagaccg	acgagacccc	gcggaccatg	ttcgacgtga	tcggcgccaa	cgcctacacc	540
atcgggggggc	gcagccgctg	ctcgatcggt	ttcgccgtca	acggcggtt	catcaccgccc	600
ggccactgcg	gccgcacccgg	cgccaccacc	gccaacccca	ccgggaccc	cgcgggtcc	660
agcttcccg	gcaacgacta	cgcgttcgtc	cgtaccgggg	ccggcgtgaa	cctcgccgtcc	720

caggtaaca	actactccgg	tggccgcgtc	caggtcgccg	ggcacaccgc	ggcccccgtc	780
ggctcgccg	tgtgccggtc	cgggtcgacc	acccgggtggc	actgcggcac	catcaactgcg	840
ctcaactcct	cgttccaccta	ccccgagggc	accgtcccg	gcctgatccg	caccaccgtc	900
tgcggccgagc	ccggcgactc	cggtggtcg	ctgtcgccg	gcaaccaggc	ccagggcgtc	960
acgtccggcg	gtccggcaa	ctgcccacc	ggtggcacca	cgtttcttcca	gcccgtcaac	1020
cccatctcc	aggcgtaacgg	cctgaggatg	atcaccacgg	actcgggcag	cagcccgccc	1080
cctgcaccga	ccttcctgcac	cggctacgccc	cgcaccttca	ccgggaccct	cgccggccggc	1140
cgggccgccc	cccagcccaa	cgggtcttac	gtgcagggtca	accgtccgg	gaccacacgc	1200
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<212> DNA  
<213> *Cellulomonas* spp.

<210> 5  
<211> 83  
<212> DNA  
<213> Cellulomonas strain 69B4

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<210> 6  
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<212> PRT  
<213> Cellulomonas strain 69B4

<400> 6

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Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala Glu Lys Leu Asp
35          40          45
Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp Ala Glu
50          55          60
Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu Thr Gly
65          70          75          80
Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr Trp Val

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85	90	95
Glu Asp Asp Val Leu Tyr Val Ala Thr	Asp Glu Asp Ala Val Glu	
100	105	110
Glu Val Glu Gly Glu Gly Ala Thr	Ala Val Thr Val Glu His Ser Leu	
115	120	125
Ala Asp Leu Glu Ala Trp Lys	Thr Val Leu Asp Ala Ala Leu Glu Gly	
130	135	140
His Asp Asp Val Pro Thr Trp Tyr Val Asp Val	Pro Thr Asn Ser Val	
145	150	155
Val Val Ala Val Lys Ala Gly Ala Gln Asp Val	Ala Ala Gly Leu Val	
165	170	175
Glu Gly Ala Asp Val Pro Ser Asp Ala Val	Thr Phe Val Glu Thr Asp	

180	185	190
Glu Thr Pro Arg Thr Met Phe Asp Val Ile	Gly Gly Asn Ala Tyr Thr	
195	200	205
Ile Gly Gly Arg Ser Arg Cys Ser Ile	Gly Phe Ala Val Asn Gly Gly	
210	215	220
Phe Ile Thr Ala Gly His Cys Gly Arg	Thr Gly Ala Thr Thr Ala Asn	
225	230	235
Pro Thr Gly Thr Phe Ala Gly Ser Ser	Phe Pro Gly Asn Asp Tyr Ala	
245	250	255
Phe Val Arg Thr Gly Ala Gly Val Asn	Leu Ala Gln Val Asn Asn	
260	265	270
Tyr Ser Gly Gly Arg Val Gln Val Ala	Gly His Thr Ala Ala Pro Val	
275	280	285
Gly Ser Ala Val Cys Arg Ser Gly Ser	Thr Thr Gly Trp His Cys Gly	
290	295	300
Thr Ile Thr Ala Leu Asn Ser Ser Val	Thr Tyr Pro Glu Gly Thr Val	
305	310	315
Arg Gly Leu Ile Arg Thr Thr Val Cys	Ala Glu Pro Gly Asp Ser Gly	
325	330	335
Gly Ser Leu Leu Ala Gly Asn Gln Ala	Gln Gly Val Thr Ser Gly Gly	
340	345	350
Ser Gly Asn Cys Arg Thr Gly Thr	Phe Phe Gln Pro Val Asn	
355	360	365
Pro Ile Leu Gln Ala Tyr Gly Leu Arg	Met Ile Thr Thr Asp Ser Gly	
370	375	380
Ser Ser Pro Ala Pro Ala Pro Thr	Ser Cys Thr Gly Tyr Ala Arg Thr	
385	390	395
Phe Thr Gly Thr Leu Ala Ala Gly Arg	Ala Ala Gln Pro Asn Gly	
405	410	415
Ser Tyr Val Gln Val Asn Arg Ser	Gly Thr His Ser Val Cys Leu Asn	
420	425	430
Gly Pro Ser Gly Ala Asp Phe Asp	Leu Tyr Val Gln Arg Trp Asn Gly	
435	440	445
Ser Ser Trp Val Thr Val Ala Gln Ser	Thr Ser Pro Gly Ser Asn Glu	
450	455	460
Thr Ile Thr Tyr Arg Gly Asn Ala Gly	Tyr Tyr Arg Tyr Val Val Asn	
465	470	475
Ala Ala Ser Gly Ser Gly Ala Tyr Thr	Met Gly Leu Thr Leu Pro	
485	490	495

<210> 7  
<211> 467  
<212> PRT

<213> Cellulomonas strain 69B4

<400> 7

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Glu Lys Leu Asp Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly  
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Leu Asp Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala  
35 40 45  
Ala Glu Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala  
50 55 60  
Gly Thr Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu  
65 70 75 80  
Asp Ala Val Glu Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val  
85 90 95  
Glu His Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala  
100 105 110  
Ala Leu Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro  
115 120 125  
Thr Asn Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala  
130 135 140  
Ala Gly Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe  
145 150 155 160  
Val Glu Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly  
165 170 175  
Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala  
180 185 190  
Val Asn Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala  
195 200 205  
Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly  
210 215 220  
Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala  
225 230 235 240  
Gln Val Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr  
245 250 255  
Ala Ala Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly  
260 265 270  
Trp His Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro  
275 280 285  
Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro  
290 295 300  
Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val  
305 310 315 320  
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe  
325 330 335  
Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr  
340 345 350  
Thr Asp Ser Gly Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly  
355 360 365  
Tyr Ala Arg Thr Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala  
370 375 380  
Gln Pro Asn Gly Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser  
385 390 395 400  
Val Cys Leu Asn Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln  
405 410 415  
Arg Trp Asn Gly Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro

420 425 430  
Gly Ser Asn Glu Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg  
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Tyr Val Val Asn Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu  
450 455 460  
Thr Leu Pro  
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<210> 8  
<211> 189  
<212> PRT  
<213> Cellulomonas spp.

<400> 8

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Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His  
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Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala  
35 40 45  
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala  
50 55 60  
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val  
65 70 75 80  
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg  
85 90 95  
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn  
100 105 110  
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr  
115 120 125  
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly  
130 135 140  
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr  
145 150 155 160  
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr  
165 170 175  
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro  
180 185

<210> 9  
<211> 28  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 9

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Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala  
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<210> 10  
<211> 23  
<212> DNA  
<213> Artificial Sequence

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 <222> (3)..(3)  
 <223> n is a, c, g, or t  
  
 <400> 10  
 acnacsggst ggcrtgtcgg cac 23

<210> 11  
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 <213> Artificial Sequence

<220>  
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 <223> n is a, c, g, or t

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<210> 12  
 <211> 58  
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 <213> Cellulomonas strain 69B4

<400> 12

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				20				25					30		
Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Leu	Ala	Gly	Asn	Gln	Ala	Gln
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Gly	Val	Thr	Ser	Gly	Asp	Ser	Gly	Gly	Ser						

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 <212> DNA  
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<210> 14  
 <211> 32

<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 14

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32

<210> 15

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 15

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33

<210> 16

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> primer

<400> 16

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34

<210> 17

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> N-terminus of the mature chain determined by MALDI-TOF analysis

<400> 17

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<210> 18

<211> 189

<212> PRT

<213> Cellulomonas strain 69B4

<400> 18

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1 . . . . . 5 . . . . . 10 . . . . . 15  
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His  
20 . . . . . 25 . . . . . 30  
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala

35	40	45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala		
50	55	60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val		
65	70	75
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg		
85	90	95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn		
100	105	110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr		
115	120	125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly		
130	135	140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr		
145	150	155
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr		
165	170	175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro		
180	185	

<210> 19  
<211> 184

<212> PRT  
<213> Streptomyces griseus

<400> 19

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20	25	30
Thr Ala Gly His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr		
35	40	45
Arg Thr Gly Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His		
50	55	60
Ser Asn Pro Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser		
65	70	75
Tyr Gln Asp Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val		
85	90	95
Gln Arg Ser Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly		
100	105	110
Leu Asn Ala Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met		
115	120	125
Ile Gln Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu		
130	135	140
Phe Ala Gly Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn		
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Cys Arg Thr Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu		
165	170	175
Ser Ala Tyr Gly Ala Thr Val Leu		
180		

<210> 20  
<211> 174  
<212> PRT  
<213> Streptomyces fradiae

<400> 20  
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20 25 30  
Ala Gly His Cys Thr Glu Ile Ala Ser Thr Trp Tyr Thr Asn Ser Gly  
35 40 45  
Gln Thr Ser Leu Leu Gly Thr Arg Ala Gly Thr Ser Phe Pro Gly Asn  
50 55 60  
Asp Tyr Gly Leu Ile Arg His Ser Asn Ala Ser Ala Ala Asp Gly Arg  
65 70 75 80  
Val Tyr Leu Tyr Asn Gly Ser Tyr Arg Asp Ile Thr Gly Ala Gly Asn  
85 90 95  
Ala Tyr Val Gly Gln Thr Val Gln Arg Ser Gly Ser Thr Thr Gly Leu  
100 105 110  
His Ser Gly Arg Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly  
115 120 125  
Gly Asp Ile Val Ser Gly Leu Ile Gln Thr Asn Val Cys Ala Glu Pro  
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Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Ser Thr Ala Leu Gly Leu  
145 150 155 160  
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr  
165 170

<210> 21  
<211> 188  
<212> PRT  
<213> Streptomyces lividans

<400> 21  
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Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser  
35 40 45  
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly  
50 55 60  
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly  
65 70 75 80  
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly  
85 90 95  
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg  
100 105 110  
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val Val  
115 120 125  
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly  
130 135 140  
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly  
145 150 155 160  
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val  
165 170 175  
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr  
180 185

<210> 22  
<211> 188  
<212> PRT  
<213> Streptomyces coelicolor

<400> 22

Asn Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg  
1 5 10 15  
Cys Ser Leu Gly Phe Asn Val Arg Thr Ser Ser Gly Ala Glu Tyr Phe  
20 25 30  
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser  
35 40 45  
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly  
50 55 60  
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly  
65 70 75 80  
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly  
85 90 95  
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg  
100 105 110  
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val Val  
115 120 125  
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly  
130 135 140  
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly  
145 150 155 160  
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val  
165 170 175  
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr  
180 185

<210> 23  
<211> 189  
<212> PRT

<213> Streptomyces albogriseolus

<400> 23

Thr Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg  
1 5 10 15  
Cys Ser Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Val Asp Tyr Phe  
20 25 30  
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Thr Trp Tyr Ser Asn  
35 40 45  
Ser Ala Arg Thr Thr Ala Ile Gly Ser Thr Ala Gly Ser Ser Phe Pro  
50 55 60  
Gly Asn Asp Tyr Gly Ile Val Arg Tyr Thr Gly Ser Val Ser Arg Pro  
65 70 75 80  
Gly Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val  
85 90 95  
Gly Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly  
100 105 110  
Arg Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Ile  
115 120 125  
Val Ser Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser

130                    135                    140  
Gly Gly Pro Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser  
145                    150                    155                    160  
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro  
                      165                    170                    175  
Val Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr  
                      180                    185

<210> 24  
<211> 188  
<212> PRT  
<213> Streptomyces griseus

<400> 24

Thr Lys Leu Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg  
1                    5                    10                    15  
Cys Ser Leu Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu  
                      20                    25                    30  
Thr Ala Gly His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser  
                      35                    40                    45  
Ala Arg Thr Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn  
                      50                    55                    60  
Asn Asp Tyr Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp  
65                    70                    75                    80  
Gly Thr Val Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val  
                      85                    90                    95  
Gly Met Ala Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly  
                      100                  105                  110  
Ser Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val  
                      115                  120                  125  
Val Tyr Gly Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser  
                      130                  135                  140  
Gly Gly Pro Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly  
145                    150                    155                    160  
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val  
                      165                  170                  175  
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr  
                      180                  185

<210> 25  
<211> 188  
<212> PRT  
<213> Streptomyces griseus

<400> 25

Val Leu Gly Gly Gly Ala Ile Tyr Gly Gly Ser Arg Cys Ser Ala  
1                    5                    10                    15  
Ala Phe Asn Val Thr Lys Gly Gly Ala Arg Tyr Phe Val Thr Ala Gly  
                      20                    25                    30  
His Cys Thr Asn Ile Ser Ala Asn Trp Ser Ala Ser Ser Gly Gly Ser  
                      35                    40                    45  
Val Val Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn Asp Tyr Gly  
                      50                    55                    60  
Ile Val Arg Tyr Thr Asp Gly Ser Ser Pro Ala Gly Thr Val Asp Leu  
65                    70                    75                    80

Tyr Asn Gly Ser Thr Gln Asp Ile Ser Ser Ala Ala Asn Ala Val Val  
                   85                  90                  95  
 Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly  
                   100              105                  110  
 Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val  
                   115              120                  125  
 Tyr Asn Met Gly Arg Thr Thr Ala Cys Ser Ala Gly Gly Asp Ser Gly  
                   130              135                  140  
 Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His Ser Gly Ser  
                   145              150                  155                  160  
 Ser Gly Cys Ser Gly Thr Ala Gly Ser Ala Ile His Gln Pro Val Thr  
                   165              170                  175  
 Lys Ala Leu Ser Ala Tyr Gly Val Thr Val Tyr Leu  
                   180              185

<210> 26  
 <211> 190  
 <212> PRT  
 <213> Streptomyces fradiae

<400> 26

Gln Arg Glu Val Ala Gly Gly Asp Ala Ile Tyr Gly Gly Ser Arg  
 1                  5                  10                  15  
 Cys Ser Ala Ala Phe Asn Val Thr Lys Asn Gly Val Arg Tyr Phe Leu  
                   20              25                  30  
 Thr Ala Gly His Cys Thr Asn Leu Ser Ser Thr Trp Ser Ser Thr Ser  
                   35              40                  45  
 Gly Gly Thr Ser Ile Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn  
                   50              55                  60  
 Asp Tyr Gly Ile Val Arg Tyr Thr Thr Thr Asn Val Asp Gly Arg  
                   65              70                  75                  80  
 Val Asn Leu Tyr Asn Gly Gly Tyr Gln Asp Ile Ala Ser Ala Ala Asp  
                   85              90                  95  
 Ala Val Val Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val  
                   100            105                  110  
 Thr Ser Gly Thr Val Ser Ala Val Asn Val Thr Val Asn Tyr Ser Asp  
                   115            120                  125  
 Gly Pro Val Tyr Gly Met Val Arg Thr Thr Ala Cys Ser Ala Gly Gly  
                   130            135                  140  
 Asp Ser Gly Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His  
                   145            150                  155                  160  
 Ser Gly Ser Ser Gly Cys Thr Gly Thr Asn Gly Ser Ala Ile His Gln  
                   165            170                  175  
 Pro Val Arg Glu Ala Leu Ser Ala Tyr Gly Val Asn Val Tyr  
                   180            185                  190

<210> 27  
 <211> 190  
 <212> PRT  
 <213> Streptomyces albogriseolus

<400> 27

Lys Pro Phe Ile Ala Gly Gly Asp Ala Ile Thr Gly Asn Gly Gly Arg  
 1                  5                  10                  15  
 Cys Ser Leu Gly Phe Asn Val Thr Lys Gly Gly Glu Pro His Phe Leu

20	25	30	
Thr Ala Gly His Cys Thr Glu Gly Ile Ser Thr Trp Ser Asp Ser Ser			
35	40	45	
Gly Gln Val Ile Gly Glu Asn Ala Ala Ser Ser Phe Pro Gly Asp Asp			
50	55	60	
Tyr Gly Leu Val Lys Tyr Thr Ala Asp Val Ala His Pro Ser Gln Val			
65	70	75	80
Asn Leu Tyr Asp Gly Ser Ser Gln Ser Ile Ser Gly Ala Ala Glu Ala			
85	90	95	
Ala Val Gly Met Gln Val Thr Arg Ser Gly Ser Thr Thr Gln Val His			
100	105	110	
Ser Gly Thr Val Thr Gly Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly			
115	120	125	
Asp Ile Val Asn Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly			
130	135	140	
Asp Ser Gly Gly Ser Leu Phe Ser Gly Asp Lys Ala Val Gly Leu Thr			
145	150	155	160
Ser Gly Gly Ser Gly Asp Cys Thr Ser Gly Gly Thr Thr Phe Phe Gln			
165	170	175	
Pro Val Thr Glu Ala Leu Ser Ala Thr Gly Thr Gln Ile Gly			
180	185	190	

<210> 28

<211> 190

<212> PRT

<213> Streptomyces coelicolor

<400> 28

Lys Pro Phe Val Ala Gly Gly Asp Ala Ile Thr Gly Gly Gly Arg			
1	5	10	15
Cys Ser Leu Gly Phe Asn Val Thr Lys Gly Gly Glu Pro Tyr Phe Ile			
20	25	30	
Thr Ala Gly His Cys Thr Glu Ser Ile Ser Thr Trp Ser Asp Ser Ser			
35	40	45	
Gly Asn Val Ile Gly Glu Asn Ala Ala Ser Ser Phe Pro Asp Asn Asp			
50	55	60	
Tyr Gly Leu Val Lys Tyr Thr Ala Asp Val Asp His Pro Ser Glu Val			
65	70	75	80
Asn Leu Tyr Asn Gly Ser Ser Gln Ala Ile Ser Gly Ala Ala Glu Ala			
85	90	95	
Thr Val Gly Met Gln Val Thr Arg Ser Gly Ser Thr Thr Gln Val His			
100	105	110	
Asp Gly Thr Val Thr Gly Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly			
115	120	125	
Asp Ile Val Asn Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly			
130	135	140	
Asp Ser Gly Gly Ser Leu Phe Ser Gly Asp Gln Ala Ile Gly Leu Thr			
145	150	155	160
Ser Gly Gly Ser Gly Asp Cys Thr Ser Gly Gly Glu Thr Phe Phe Gln			
165	170	175	
Pro Val Thr Glu Ala Leu Ser Ala Thr Gly Thr Gln Ile Gly			
180	185	190	

<210> 29

<211> 191

<212> PRT

<213> Streptomyces griseus

<400> 29

Thr Pro Leu Ile Ala Gly Gly Asp Ala Ile Trp Gly Ser Gly Ser Arg  
1 5 10 15  
Cys Ser Leu Gly Phe Asn Val Val Lys Gly Gly Glu Pro Tyr Phe Leu  
20 25 30  
Thr Ala Gly His Cys Thr Glu Ser Val Thr Ser Trp Ser Asp Thr Gln  
35 40 45  
Gly Gly Ser Glu Ile Gly Ala Asn Glu Gly Ser Ser Phe Pro Glu Asn  
50 55 60  
Asp Tyr Gly Leu Val Lys Tyr Thr Ser Asp Thr Ala His Pro Ser Glu  
65 70 75 80  
Val Asn Leu Tyr Asp Gly Ser Thr Gln Ala Ile Thr Gln Ala Gly Asp  
85 90 95  
Ala Thr Val Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val  
100 105 110  
His Asp Gly Glu Val Thr Ala Leu Asp Ala Thr Val Asn Tyr Gly Asn  
115 120 125  
Gly Asp Ile Val Asn Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro  
130 135 140  
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Asp Thr Ala Leu Gly Leu  
145 150 155 160  
Thr Ser Gly Gly Ser Gly Asp Cys Ser Ser Gly Gly Thr Thr Phe Phe  
165 170 175  
Gln Pro Val Pro Glu Ala Leu Ala Ala Tyr Gly Ala Glu Ile Gly  
180 185 190

<210> 30

<211> 200

<212> PRT

<213> Streptomyces lividans

<400> 30

Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Ala Arg  
1 5 10 15  
Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Ala Ala Phe  
20 25 30  
Leu Thr Arg Gly His Cys Gly Gly Ala Thr Met Trp Ser Asp Ala  
35 40 45  
Gln Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Pro  
50 55 60  
Glu Gly Asp Phe Gly Leu Val Arg Tyr Asp Gly Pro Ser Thr Glu Ala  
65 70 75 80  
Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala  
85 90 95  
Ala Glu Ala Ser Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr  
100 105 110  
Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Val Thr Val Asn Tyr  
115 120 125  
Pro Glu Gly Thr Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu  
130 135 140  
Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile  
145 150 155 160  
Arg Leu Thr Ser Gly Gly Thr Arg Asp Cys Thr Ser Gly Gly Glu Thr

165 170 175  
Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Gly Thr Leu  
180 185 190  
Gly Gly Glu Asp Gly Gly Asp Gly  
195 200

<210> 31  
<211> 201  
<212> PRT  
<213> Streptomyces coelicolor

<400> 31

Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Ala Arg  
1 5 10 15  
Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Pro Ala Phe  
20 25 30  
Leu Thr Ala Gly His Cys Gly Val Ala Ala Asp Gln Trp Ser Asp Ala  
35 40 45  
Gln Gly Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Gly  
50 55 60  
Glu Gly Asp Phe Ala Leu Val Arg Tyr Asp Asp Pro Ala Thr Glu Ala  
65 70 75 80  
Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala  
85 90 95  
Ala Glu Ala Ala Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr  
100 105 110  
Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Ala Thr Val Asn Tyr  
115 120 125  
Pro Glu Gly Met Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu  
130 135 140  
Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile  
145 150 155 160  
Gly Leu Thr Ser Gly Gly Ser Gly Asp Cys Thr Val Gly Glu Thr  
165 170 175  
Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Ala Thr Leu  
180 185 190  
Gly Gly Glu Asp Gly Gly Ala Gly Ala  
195 200

<210> 32  
<211> 68  
<212> PRT  
<213> Streptomyces platensis

<400> 32

Val Asp Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly Asp Ser  
1 5 10 15  
Gly Gly Ala Leu Phe Asp Gly Asp Ala Ala Ile Gly Leu Thr Ser Gly  
20 25 30  
Gly Ser Gly Asp Cys Ser Gln Gly Gly Glu Thr Phe Phe Gln Pro Val  
35 40 45  
Thr Glu Ala Leu Lys Ala Tyr Gly Ala Gln Ile Gly Gly Gln Gly  
50 55 60  
Glu Pro Pro Glu  
65

<210> 33  
<211> 201  
<212> PRT  
<213> Streptomyces coelicolor

<400> 33

Thr Thr Arg Leu Asn Gly Ala Glu Pro Ile Leu Ser Thr Ala Gly Arg  
1 5 10 15  
Cys Ser Ala Gly Phe Asn Val Thr Asp Gly Thr Ser Asp Phe Ile Leu  
20 25 30  
Thr Ala Gly His Cys Gly Pro Thr Gly Ser Val Trp Phe Gly Asp Arg  
35 40 45  
Pro Gly Asp Gly Gln Val Gly Arg Thr Val Ala Gly Ser Phe Pro Gly  
50 55 60  
Asp Asp Phe Ser Leu Val Glu Tyr Ala Asn Gly Lys Ala Gly Asp Gly  
65 70 75 80  
Ala Asp Val Val Ala Val Gly Asp Gly Lys Gly Val Arg Ile Thr Gly  
85 90 95  
Ala Gly Glu Pro Ala Val Gly Gln Arg Val Phe Arg Ser Gly Ser Thr  
100 105 110  
Ser Gly Leu Arg Asp Gly Arg Val Thr Ala Leu Asp Ala Thr Val Asn  
115 120 125  
Tyr Pro Glu Gly Thr Val Thr Gly Leu Ile Glu Thr Asp Val Cys Ala  
130 135 140  
Glu Pro Gly Asp Ser Gly Gly Pro Met Phe Ser Glu Gly Val Ala Leu  
145 150 155 160  
Gly Val Thr Ser Gly Gly Ser Gly Asp Cys Ala Lys Gly Thr Thr  
165 170 175  
Phe Phe Gln Pro Leu Pro Glu Ala Met Ala Ser Leu Gly Val Arg Leu  
180 185 190  
Ile Val Pro Gly Arg Glu Gly Ala Ala  
195 200

<210> 34  
<211> 188  
<212> PRT  
<213> Metarhizium anisopliae

<400> 34

Ala Thr Val Gln Gly Gly Asp Val Tyr Tyr Ile Asn Arg Ser Ser Arg  
1 5 10 15  
Cys Ser Ile Gly Phe Ala Val Thr Thr Gly Phe Val Ser Ala Gly His  
20 25 30  
Cys Gly Gly Ser Gly Ala Ser Ala Thr Thr Ser Ser Gly Glu Ala Leu  
35 40 45  
Gly Thr Phe Ser Gly Ser Val Phe Pro Gly Ser Ala Asp Met Ala Tyr  
50 55 60  
Val Arg Thr Val Ser Gly Thr Val Leu Arg Gly Tyr Ile Asn Gly Tyr  
65 70 75 80  
Gly Gln Gly Ser Phe Pro Val Ser Gly Ser Ser Glu Ala Ala Val Gly  
85 90 95  
Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gln Val His Cys Gly Thr  
100 105 110  
Ile Gly Ala Lys Gly Ala Thr Val Asn Tyr Pro Gln Gly Ala Val Ser

115 120 125  
Gly Leu Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly  
130 135 140  
Ser Phe Tyr Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser  
145 150 155 160  
Gly Asp Cys Ser Arg Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Arg  
165 170 175  
Ile Leu Gln Thr Tyr Gly Leu Thr Leu Val Thr Ala  
180 185

<210> 35  
<211> 195  
<212> PRT  
<213> Streptomyces griseus

<400> 35

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg  
1 5 10 15  
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala  
20 25 30  
Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Asn Gly Val Asn  
35 40 45  
Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp  
50 55 60  
Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val  
65 70 75 80  
Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser  
85 90 95  
Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His  
100 105 110  
Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly  
115 120 125  
Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp  
130 135 140  
Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser  
145 150 155 160  
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro  
165 170 175  
Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly  
180 185 190  
Gly Gly Thr  
195

<210> 36  
<211> 197  
<212> PRT  
<213> Streptomyces coelicolor

<400> 36

Tyr Asp Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg  
1 5 10 15  
Cys Ser Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala  
20 25 30  
Thr Ala Gly His Cys Gly Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn  
35 40 45

Arg Val Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp  
50 55 60  
Met Ala Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val  
65 70 75 80  
Leu Gly Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser  
85 90 95  
Pro Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His  
100 105 110  
Cys Gly Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly  
115 120 125  
Thr Ile Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp  
130 135 140  
Ser Gly Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser  
145 150 155 160  
Gly Gly Ser Gly Asp Cys Arg Thr Gly Gly Glu Thr Phe Phe Gln Pro  
165 170 175  
Ile Asn Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly  
180 185 190  
Gly Asp Asp Gly Gly  
195

<210> 37  
<211> 189  
<212> PRT  
<213> Streptomyces spp.

<400> 37

Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Ile Gly Asn Gly Arg Cys  
1 5 10 15  
Ser Ile Gly Phe Ser Val Arg Gln Gly Ser Thr Pro Gly Phe Val Thr  
20 25 30  
Ala Gly His Cys Gly Ser Val Gly Asn Ala Thr Thr Gly Phe Asn Arg  
35 40 45  
Val Ser Gln Gly Thr Phe Arg Gly Ser Trp Phe Pro Gly Arg Asp Met  
50 55 60  
Ala Trp Val Ala Val Asn Ser Asn Trp Thr Pro Thr Ser Leu Val Arg  
65 70 75 80  
Asn Ser Gly Ser Gly Val Arg Val Thr Gly Ser Thr Gln Ala Thr Val  
85 90 95  
Gly Ser Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly  
100 105 110  
Thr Ile Gln Gln His Asn Thr Ser Val Thr Tyr Pro Gln Gly Thr Ile  
115 120 125  
Thr Gly Val Thr Arg Thr Ser Ala Cys Ala Gln Pro Gly Asp Ser Gly  
130 135 140  
Gly Ser Phe Ile Ser Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly  
145 150 155 160  
Ser Gly Asn Cys Ser Ile Gly Gly Thr Thr Phe His Gln Pro Val Asn  
165 170 175  
Pro Ile Leu Ser Gln Tyr Gly Leu Thr Leu Val Arg Ser  
180 185

<210> 38  
<211> 187  
<212> PRT  
<213> Streptomyces spp.

<400> 38

Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Met Gly Gly Gly Arg Cys  
1 5 10 15  
Ser Val Gly Phe Ser Val Thr Gln Gly Ser Thr Pro Gly Phe Ala Thr  
20 25 30  
Ala Gly His Cys Gly Thr Val Gly Thr Ser Thr Thr Gly Tyr Asn Gln  
35 40 45  
Ala Ala Gln Gly Thr Phe Glu Glu Ser Ser Phe Pro Gly Asp Asp Met  
50 55 60  
Ala Trp Val Ser Val Asn Ser Asp Trp Asn Thr Thr Pro Thr Val Asn  
65 70 75 80  
Glu Gly Glu Val Thr Val Ser Gly Ser Thr Glu Ala Ala Val Gly Ala  
85 90 95  
Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile  
100 105 110  
Gln Gln His Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr Ile Thr Gly  
115 120 125  
Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser  
130 135 140  
Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly  
145 150 155 160  
Asn Cys Thr Ser Gly Gly Thr Thr Tyr His Gln Pro Ile Asn Pro Leu  
165 170 175  
Leu Ser Ala Tyr Gly Leu Asp Leu Val Thr Gly  
180 185

<210> 39

<211> 193

<212> PRT

<213> Streptomyces coelicolor

<400> 39

Glu Asp Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg  
1 5 10 15  
Cys Ser Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala  
20 25 30  
Thr Ala Gly His Cys Gly Asp Pro Gly Ala Thr Thr Gly Tyr Asn  
35 40 45  
Glu Ala Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp  
50 55 60  
Met Ala Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val  
65 70 75 80  
Lys Ala Glu Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala  
85 90 95  
Leu Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His  
100 105 110  
Cys Gly Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly  
115 120 125  
Thr Val Asp Gly Leu Thr Glu Thr Thr Val Cys Ala Glu Pro Gly Asp  
130 135 140  
Ser Gly Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser  
145 150 155 160  
Gly Gly Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro  
165 170 175

Val Asn Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser  
180 185 190

Ala

<210> 40

<211> 187

<212> PRT

<213> Thermobifida fusca

<400> 40

Leu Ala Ala Ile Ile Gly Gly Asn Pro Tyr Tyr Phe Gly Asn Tyr Arg  
1 5 10 15  
Cys Ser Ile Gly Phe Ser Val Arg Gln Gly Ser Gln Thr Gly Phe Ala  
20 25 30  
Thr Ala Gly His Cys Gly Ser Thr Gly Thr Arg Val Ser Ser Pro Ser  
35 40 45  
Gly Thr Val Ala Gly Ser Tyr Phe Pro Gly Arg Asp Met Gly Trp Val  
50 55 60  
Arg Ile Thr Ser Ala Asp Thr Val Thr Pro Leu Val Asn Arg Tyr Asn  
65 70 75 80  
Gly Gly Thr Val Thr Val Thr Gly Ser Gln Glu Ala Ala Thr Gly Ser  
85 90 95  
Ser Val Cys Arg Ser Gly Ala Thr Thr Gly Trp Arg Cys Gly Thr Ile  
100 105 110  
Gln Ser Lys Asn Gln Thr Val Arg Tyr Ala Glu Gly Thr Val Thr Gly  
115 120 125  
Leu Thr Arg Thr Thr Ala Cys Ala Glu Gly Gly Asp Ser Gly Gly Pro  
130 135 140  
Trp Leu Thr Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Thr Gly  
145 150 155 160  
Asp Cys Arg Ser Gly Gly Ile Thr Phe Phe Gln Pro Ile Asn Pro Leu  
165 170 175  
Leu Ser Tyr Phe Gly Leu Gln Leu Val Thr Gly  
180 185

<210> 41

<211> 198

<212> PRT

<213> Lysobacter enzymogenes

<400> 41

Ala Asn Ile Val Gly Gly Ile Glu Tyr Ser Ile Asn Asn Ala Ser Leu  
1 5 10 15  
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Ala Thr Lys Gly Phe Val  
20 25 30  
Thr Ala Gly His Cys Gly Thr Val Asn Ala Thr Ala Arg Ile Gly Gly  
35 40 45  
Ala Val Val Gly Thr Phe Ala Ala Arg Val Phe Pro Gly Asn Asp Arg  
50 55 60  
Ala Trp Val Ser Leu Thr Ser Ala Gln Thr Leu Leu Pro Arg Val Ala  
65 70 75 80  
Asn Gly Ser Ser Phe Val Thr Val Arg Gly Ser Thr Glu Ala Ala Val  
85 90 95  
Gly Ala Ala Val Cys Arg Ser Gly Arg Thr Thr Gly Tyr Gln Cys Gly

	100	105	110
Thr Ile Thr Ala Lys Asn Val Thr Ala Asn Tyr Ala Glu Gly Ala Val			
115	120	125	
Arg Gly Leu Thr Gln Gly Asn Ala Cys Met Gly Arg Gly Asp Ser Gly			
130	135	140	
Gly Ser Trp Ile Thr Ser Ala Gly Gln Ala Gln Gly Val Met Ser Gly			
145	150	155	160
Gly Asn Val Gln Ser Asn Gly Asn Asn Cys Gly Ile Pro Ala Ser Gln			
165	170	175	
Arg Ser Ser Leu Phe Glu Arg Leu Gln Pro Ile Leu Ser Gln Tyr Gly			
180	185	190	
Leu Ser Leu Val Thr Gly			
195			

<210> 42

<211> 189

<212> PRT

<213> Streptomyces coelicolor

<400> 42

Ala Ala Gly Thr Val Gly Gly Asp Pro Tyr Tyr Thr Gly Asn Val Arg			
1	5	10	15
Cys Ser Ile Gly Phe Ser Val His Gly Gly Phe Val Thr Ala Gly His			
20	25	30	
Cys Gly Arg Ala Gly Ala Gly Val Ser Gly Trp Asp Arg Ser Tyr Ile			
35	40	45	
Gly Thr Phe Gln Gly Ser Ser Phe Pro Asp Asn Asp Tyr Ala Trp Val			
50	55	60	
Ser Val Gly Ser Gly Trp Trp Thr Val Pro Val Val Leu Gly Trp Gly			
65	70	75	80
Thr Val Ser Asp Gln Leu Val Arg Gly Ser Asn Val Ala Pro Val Gly			
85	90	95	
Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr His Trp His Cys Gly Thr			
100	105	110	
Val Leu Ala His Asn Glu Thr Val Asn Tyr Ser Asp Gly Ser Val Val			
115	120	125	
His Gln Leu Thr Lys Thr Ser Val Cys Ala Glu Gly Gly Asp Ser Gly			
130	135	140	
Gly Ser Phe Ile Ser Gly Asp Gln Ala Gln Gly Val Thr Ser Gly Gly			
145	150	155	160
Trp Gly Asn Cys Ser Ser Gly Gly Glu Thr Trp Phe Gln Pro Val Asn			
165	170	175	
Glu Ile Leu Asn Arg Tyr Gly Leu Thr Leu His Thr Ala			
180	185		

<210> 43

<211> 197

<212> PRT

<213> Rarobacter faecitabidus

<400> 43

Val Ile Val Pro Val Arg Asp Tyr Trp Gly Gly Asp Ala Leu Ser Gly			
1	5	10	15
Cys Thr Leu Ala Phe Pro Val Tyr Gly Gly Phe Leu Thr Ala Gly His			
20	25	30	

Cys Ala Val Glu Gly Lys Gly His Ile Leu Lys Thr Glu Met Thr Gly  
35 40 45  
Gly Gln Ile Gly Thr Val Glu Ala Ser Gln Phe Gly Asp Gly Ile Asp  
50 55 60  
Ala Ala Trp Ala Lys Asn Tyr Gly Asp Trp Asn Gly Arg Gly Arg Val  
65 70 75 80  
Thr His Trp Asn Gly Gly Gly Val Asp Ile Lys Gly Ser Asn Glu  
85 90 95  
Ala Ala Val Gly Ala His Met Cys Lys Ser Gly Arg Thr Thr Lys Trp  
100 105 110  
Thr Cys Gly Tyr Leu Leu Arg Lys Asp Val Ser Val Asn Tyr Gly Asn  
115 120 125  
Gly His Ile Val Thr Leu Asn Glu Thr Ser Ala Cys Ala Leu Gly Gly  
130 135 140  
Asp Ser Gly Gly Ala Tyr Val Trp Asn Asp Gln Ala Gln Gly Ile Thr  
145 150 155 160  
Ser Gly Ser Asn Met Asp Thr Asn Asn Cys Arg Ser Phe Tyr Gln Pro  
165 170 175  
Val Asn Thr Val Leu Asn Lys Trp Lys Leu Ser Leu Val Thr Ser Thr  
180 185 190  
Asp Val Thr Thr Ser  
195

<210> 44

<211> 191

<212> PRT

<213> Streptomyces coelicolor

<400> 44

Asp Pro Pro Leu Arg Ser Gly Leu Ala Ile Tyr Gly Thr Asn Val Arg  
1 5 10 15  
Cys Ser Ser Ala Phe Met Ala Tyr Ser Gly Ser Ser Tyr Tyr Met Met  
20 25 30  
Thr Ala Gly His Cys Ala Glu Asp Ser Ser Tyr Trp Glu Val Pro Thr  
35 40 45  
Tyr Ser Tyr Gly Tyr Gln Gly Val Gly His Val Ala Asp Tyr Thr Phe  
50 55 60  
Gly Tyr Tyr Gly Asp Ser Ala Ile Val Arg Val Asp Asp Pro Gly Phe  
65 70 75 80  
Trp Gln Pro Arg Gly Trp Val Tyr Pro Ser Thr Arg Ile Thr Asn Trp  
85 90 95  
Asp Tyr Asp Tyr Val Gly Gln Tyr Val Cys Lys Gln Gly Ser Thr Thr  
100 105 110  
Gly Tyr Thr Cys Gly Gln Ile Thr Glu Thr Asn Ala Thr Val Ser Tyr  
115 120 125  
Pro Gly Arg Thr Leu Thr Gly Met Thr Trp Ser Thr Ala Cys Asp Ala  
130 135 140  
Pro Gly Asp Ser Gly Ser Gly Val Tyr Asp Gly Ser Thr Ala His Gly  
145 150 155 160  
Ile Leu Ser Gly Gly Pro Asn Ser Gly Cys Gly Met Ile His Glu Pro  
165 170 175  
Ile Ser Arg Ala Leu Ala Asp Arg Gly Val Thr Leu Leu Ala Gly  
180 185 190

<210> 45

<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 45  
tgcgccgagc ccggcgactc 20

<210> 46  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 46  
gagtcgcccc gctcggcgca 20

<210> 47  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 47  
ttcccccggca acgactacgc gtgggt 26

<210> 48  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 48  
accCACGCGT agtcgttgcc ggggaa 26

<210> 49  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 49  
gccgctgctc gatcgggttc 20

<210> 50  
<211> 24

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 50  
 gcagttgccg gagccggcgg acgt 24

<210> 51  
 <211> 14  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> synthetic

<220>  
 <221> misc\_feature  
 <222> (7)...(7)  
 <223> n is a, c, g, or t

<400> 51  
 tsoggsgnncrt ggtt 14

<210> 52  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic

<400> 52

Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro  
 1 5 10

<210> 53  
 <211> 555  
 <212> DNA  
 <213> Cellulomonas flavigena

<400> 53  
 gtgcacgtca tcggggcaa cgctactac atcgggtcg gctcgccgtg ctgcgtcg 60  
 ttccgcgtcg agggcggtt cgtcaccgcg gggcactgcg ggcgcgcggg cgcgagcacg 120  
 tcgtcaccgt cggggacctt ccgcggctcg tcgtccccg gcaacgacta cgcgtggtc 180  
 caggtcgct cgggcaaacac gcccgcggg ctggtaaca accactcggg cggcacggtg 240  
 cgcgtcaccg gctcgacga ggcgcgcggc ggctcgatc tgtgccgatc gggcagcacg 300  
 acgggatggc ggtcgcccta cgtccggcg tacaacacga ccgtcggtt cgcggaggc 360  
 tcggtctcg gctcatccg cacgagcgtg tgccgcgagc cggcgactc cggccgctcg 420  
 ctgtcgccg gcacgcaggc ccaggcggtc acgtcggcg ggtccggcaa ctgcccgtac 480  
 gggggcacga cgtacttcca gcccgtgaac gagatcctgc aggaccagcc cggccgctcg 540  
 accacgcgtg cccta 555

<210> 54  
 <211> 185  
 <212> PRT  
 <213> Cellulomonas flavigena

<400> 54

Val Asp Val Ile Gly Gly Asn Ala Tyr Tyr Ile Gly Ser Arg Ser Arg  
 1 5 10 15  
 Cys Ser Ile Gly Phe Ala Val Glu Gly Gly Phe Val Thr Ala Gly His  
 20 25 30  
 Cys Gly Arg Ala Gly Ala Ser Thr Ser Ser Pro Ser Gly Thr Phe Arg  
 35 40 45  
 Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Ala Ser  
 50 55 60  
 Gly Asn Thr Pro Arg Gly Leu Val Asn Asn His Ser Gly Gly Thr Val  
 65 70 75 80  
 Arg Val Thr Gly Ser Gln Gln Ala Ala Val Gly Ser Tyr Val Cys Arg  
 85 90 95  
 Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Tyr Val Arg Ala Tyr Asn  
 100 105 110  
 Thr Thr Val Arg Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile Arg Thr  
 115 120 125  
 Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val Ala Gly  
 130 135 140  
 Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Tyr  
 145 150 155 160  
 Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln Asp Gln  
 165 170 175  
 Pro Gly Pro Ser Thr Thr Arg Ala Leu  
 180 185

<210> 55  
 <211> 1009  
 <212> DNA  
 <213> Cellulomonas biazotea

<400> 55

taaaacagac ggccagtgaa tttgtataac gactcactat aggcgaaattt	aatttagcggtt	60
ccgcgaattt gcccttaccc atagggcacg cgtggtcgac ggccctgggc	ttgtacgtcg	120
acgtcactac caacacggtc gtcgtcaacg ccaccgcctt cgccgtggcc	caggcgaccg	180
agatcgtcgc cgccgcaacg gtgcccggcc acgcccgtccg ggtcgtcgag	accacccagg	240
cgcggccgac gttcatcgac gtcatcgccg gcaaccgtta ccggatcaac	aacacacccgc	300
gctgctcggt cggcttcgcc gtcagcgccg gcttcgtcac cgccgggcac	tgcggcacga	360
ccggcgccgac cacgacgaaa ccgtccggca cgttcggccgg ctcgtcggttc	ccccggcaacg	420
actacgcgtg ggtgcgcgtc ggtccggca acaccccggt cggccggctg	aacaactaca	480
gcggcgccgac cgtggccgtc gccggctcga cgcaggcgac cgtcggtcg	tccgtctgcc	540
gctccggctc caccacgggg tggcgctcg ggacgatcca ggcgttcaac	tccaccgtca	600
actacgcgtca gggcagcgtc tccggcctca tccgcacgaa cgtgtcgcc	gagcccgccg	660
actccggccgg ctcgtctcata gcccggcaacc aggcccagg	cctgacgtcc ggcgggtcg	720
gcaactgcac caccggccgg acgacgtact tccagccgtt	caacgaggcg ctctccgcct	780
acggcctgac gtcgtcagc tctgtccggcg gcggcggtgg	cgccggcaccg acctgcaccg	840
ggtacgcgtcg gacctacacc ggctcgctcg cctcgccgca	gtccggccgtc cagccgtccg	900
gcagctatgt gaccgtcgaa tccagcgccca ccatccgcgt	ctgcctcgac ggcccggagcg	960
ggacggactt cgacctgtac ctgcagaagt ggaacgggtc	cgcgtgggc	1009

<210> 56

<211> 335  
<212> PRT  
<213> Cellulomonas biazotea

<400> 56

Lys Gln Thr Ala Ser Glu Phe Val Ile Arg Leu Thr Ile Gly Glu Leu  
1 5 10 15  
Asn Leu Ala Ala Ala Asn Ser Pro Leu Pro Ile Gly His Ala Trp Ser  
20 25 30  
Thr Ala Leu Gly Trp Tyr Val Asp Val Thr Thr Asn Thr Val Val Val  
35 40 45  
Asn Ala Thr Ala Leu Ala Val Ala Gln Ala Thr Glu Ile Val Ala Ala  
50 55 60  
Ala Thr Val Pro Ala Asp Ala Val Arg Val Val Glu Thr Thr Glu Ala  
65 70 75 80  
Pro Arg Thr Phe Ile Asp Val Ile Gly Gly Asn Arg Tyr Arg Ile Asn  
85 90 95  
Asn Thr Ser Arg Cys Ser Val Gly Phe Ala Val Ser Gly Gly Phe Val  
100 105 110  
Thr Ala Gly His Cys Gly Thr Thr Gly Ala Thr Thr Thr Lys Pro Ser  
115 120 125  
Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val  
130 135 140  
Arg Val Ala Ser Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser  
145 150 155 160  
Gly Gly Thr Val Ala Val Ala Gly Ser Thr Gln Ala Thr Val Gly Ala  
165 170 175  
Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile  
180 185 190  
Gln Ala Phe Asn Ser Thr Val Asn Tyr Ala Gln Gly Ser Val Ser Gly

195 200 205  
Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser  
210 215 220  
Leu Ile Ala Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly  
225 230 235 240  
Asn Cys Thr Thr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala  
245 250 255  
Leu Ser Ala Tyr Gly Leu Thr Leu Val Thr Ser Ser Gly Gly Gly  
260 265 270  
Gly Gly Gly Thr Thr Cys Thr Gly Tyr Ala Arg Thr Tyr Thr Gly Ser  
275 280 285  
Leu Ala Ser Arg Gln Ser Ala Val Gln Pro Ser Gly Ser Tyr Val Thr  
290 295 300  
Val Gly Ser Ser Gly Thr Ile Arg Val Cys Leu Asp Gly Pro Ser Gly  
305 310 315 320  
Thr Asp Phe Asp Leu Tyr Leu Gln Lys Trp Asn Gly Ser Ala Trp  
325 330 335

<210> 57  
<211> 474  
<212> DNA  
<213> Cellulomonas fimi

<400> 57

gtggacgtga	tcggcgccga	cgcctactac	atcggcgccc	gcagccgctg	ttcgatcggt	60
ttcggcggtca	ccgggggtt	cgtgaccgccc	gggcactgcg	gccgcacccgg	cgcggccacg	120
acgagcccg	cgggcacgtt	cgccggctcg	agcttcccgg	gcaacgacta	cgcgtgggtg	180
cgggtcgctg	cgggcaaacac	gcccgtcgcc	gccccgtgaaca	actacagcgg	cggcacggtc	240
gcccgtcgcc	gctcgaccac	ggccgcccgtc	ggtgcgacccg	tgtgccgctc	gggctccacc	300
accggctggc	ggtgcggcac	catccaggcg	ttcaacgcga	ccgtcaacta	cgccgagggc	360
agcgtctccg	gcctcatccg	cacgaacgtg	tgcgccgagc	ccggcgactc	ggggcgctcg	420
ctcgtcgccc	gcaaccaggc	gcagggcatg	acgtccggcg	gctccgacaa	ctgc	474

<210> 58

<211> 144

<212> PRT

<213> Cellulomonas fimi

<400> 58

Val	Asp	Val	Ile	Gly	Gly	Asp	Ala	Tyr	Tyr	Ile	Gly	Gly	Arg	Ser	Arg
1				5						10			15		
Cys	Ser	Ile	Gly	Phe	Ala	Val	Thr	Gly	Gly	Phe	Val	Thr	Ala	Gly	His
				20				25				30			
Cys	Gly	Arg	Thr	Gly	Ala	Ala	Thr	Thr	Ser	Pro	Ser	Gly	Thr	Phe	Ala
		35					40				45				
Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Arg	Val	Ala	Ser
		50				55				60					
Gly	Asn	Thr	Pro	Val	Gly	Ala	Val	Asn	Asn	Tyr	Ser	Gly	Gly	Thr	Val
	65				70				75			80			
Ala	Val	Ala	Gly	Ser	Thr	Gln	Ala	Ala	Val	Gly	Ala	Thr	Val	Cys	Arg
				85				90				95			
Ser	Gly	Ser	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Thr	Ile	Gln	Ala	Phe	Asn
				100				105				110			
Ala	Thr	Val	Asn	Tyr	Ala	Glu	Gly	Ser	Val	Ser	Gly	Leu	Ile	Arg	Thr
		115				120				125					
Asn	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Val	Ala	Gly
	130				135				140						

<210> 59.

<211> 462

<212> DNA

<213> Cellulomonas gelida

<400> 59

ctcgcgccca	accaggcgca	gggcgtgacg	tcggcggtt	cgggcaactg	ctcgtcgggc	60
gggacgacgt	acttccagcc	cgtcaacgag	gccctccggg	tgtacgggct	cacgctcg	120
acctctgacg	gtggggcac	cgagccgccc	ccgacgggt	gccagggtct	tgcgcggacc	180
taccaggcga	gcgtctcgcc	cgggacgtcg	gtcgccgc	cgaacggttc	gtacgtc	240
accggggcgc	ggacgacccg	ggtgtgcctg	agcggacccgg	ccggcacgg	cctggacctg	300
tacctgcaga	agtggAACGG	gtactcg	gcccagctcg	cgca	gtcgcttg	360
gccacggagg	cggcacgt	caccgggacc	gcccgtact	accgctacgt	ggtccacgcg	420
tacgcgggtt	cggggcgta	caccctgggg	gcgacgaccc	cg		462

<210> 60

<211> 154

<212> PRT

<213> Cellulomonas gelida

<400> 60

Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn

1	5	10	15
Cys Ser Ser Gly	Gly Thr Thr Tyr	Phe Gln Pro Val Asn	Glu Ala Leu
20	25	30	
Arg Val Tyr Gly	Leu Thr Leu Val Thr Ser Asp	Gly Gly	Gly Thr Glu
35	40	45	
Pro Pro Pro Thr Gly	Cys Gln Gly Tyr Ala Arg Thr	Tyr Gln Gly	Ser
50	55	60	
Val Ser Ala Gly	Thr Ser Val Ala Gln Pro Asn	Gly Ser	Tyr Val Thr
65	70	75	80
Thr Gly Gly	Gly Thr His Arg Val Cys	Leu Ser Gly	Pro Ala Gly Thr
85	90	95	
Asp Leu Asp Leu	Tyr Leu Gln Lys Trp Asn	Gly Tyr Ser Trp	Ala Ser
100	105	110	
Val Ala Gln Ser	Thr Ser Pro Gly	Ala Thr Glu	Ala Val Thr Tyr Thr
115	120	125	
Gly Thr Ala Gly	Tyr Tyr Arg Tyr Val Val His	Ala Tyr Ala Gly Ser	
130	135	140	
Gly Ala Tyr Thr	Leu Gly Ala Thr Thr Pro		
145	150		

<210> 61  
<211> 257

<212> DNA  
<213> Cellulomonas iranensis

<400>	61					
tcccccggca	acgactacgc	gtgggtccag	gtcgggtcg	gacacacccc	ccggggcctg	60
gtcaacaact	acgcgggcgg	caccgtgcgg	gtcaccgggt	cgcagcaggc	cgcggtcg	120
gctacgtct	gccggtcggg	cagcacgacg	ggctggcgct	gcggcaccgt	gcaggcctac	180
aacgcgtcgg	tccgctacgc	cgagggcacc	gtctcggcc	tcatccgcac	caacgtctgc	240
gccgagcccg	gctactc					257

<210> 62  
<211> 85  
<212> PRT  
<213> Cellulomonas iranensis

<400> 62

Phe Pro Gly Asn Asp	Tyr Ala Trp Val Gln Val	Gly Ser Gly Asp Thr	
1	5	10	15
Pro Arg Gly	Leu Val Asn Asn Tyr Ala Gly	Gly Thr Val Arg Val Thr	
20	25	30	
Gly Ser Gln	Gln Ala Ala Val Gly	Ala Tyr Val Cys Arg Ser Gly Ser	
35	40	45	
Thr Thr Gly	Trp Arg Cys Gly	Thr Val Gln Ala Tyr Asn Ala Ser Val	
50	55	60	
Arg Tyr Ala Glu	Gly Thr Val Ser Gly	Leu Ile Arg Thr Asn Val Cys	
65	70	75	80
Ala Glu Pro	Gly Asp		
85			

<210> 63  
<211> 904  
<212> DNA  
<213> Cellulomonas cellasea

<400> 63

gtcgggcggg	tccggcaact	gccgctacgg	gggcacgacg	tacttccagc	ccgtgaacga	60
gatcctgcag	gcctacggtc	tgcgtctcg	cctgggctga	cacgctcg	gcgggcccgg	120
ctcgacgccc	ccggccccgtc	ggcccgggtc	gccgcctgg	acgtcgacgt	gccgaccaac	180
aagctcg	tcgagtcggt	cggcgacacc	gcccggccg	ccgacgcccgt	cgcgcgcg	240
ggcctgcctg	ccgacgcccgt	gacgctcg	accaccgagg	cgccacggac	tttcgtcgac	300
gtcatcg	gcaacgcgt	ctacatcaac	gcgagcagcc	gctgctcggt	cggcttcgcg	360
gtcgagggcg	ggtcgtcac	cgcgggcccac	tgcgggcgc	cggcgcgag	cacgtcgta	420
ccgtcg	ccctccgcgg	ctcgtcg	cccggcaacg	actacgcgtg	gttccagg	480
gcctcg	acacgcccgc	cgggctgg	aacaaccact	cgggcggcac	gtgcgcgtc	540
accggctcgc	agcaggccgc	gtcggcgtc	tacgtgtg	gatcggcag	cacgacgg	600
tggcgtcg	gctacgtccg	ggcgtacaac	acgaccgtc	ggtacgcg	ggctcg	660
tcggcctca	tccgcacgag	cgtgtgc	gagccggcg	actccggcg	ctcgcgt	720
gccggcacgc	aggcccagg	cgtcacgtc	ggcgggtcc	gcaactg	ctacggggc	780
acgacgtact	tccagcccgt	gaacgagatc	ctgcaggc	acggtctgc	tctcg	840
ggcgtacacg	ctcgcggcgg	gccctccct	gcccgtcg	cgccggcccc	accagcccg	900
gccc						904

<210> 64

<211> 300

<212> PRT

<213> Cellulomonas cellasea

<400> 64

Val	Gly	Arg	Val	Arg	Gln	Leu	Pro	Leu	Arg	Gly	His	Asp	Val	Leu	Pro
1					5				10					15	
Ala	Arg	Glu	Arg	Asp	Pro	Ala	Gly	Leu	Arg	Ser	Ala	Ser	Arg	Pro	Gly
						20			25					30	
Leu	Thr	Arg	Ser	Arg	Arg	Ala	Arg	Leu	Asp	Ala	Ala	Gly	Pro	Ser	Ala
						35			40					45	
Arg	Val	Ala	Ala	Trp	Tyr	Val	Asp	Val	Pro	Thr	Asn	Lys	Leu	Val	Val
						50			55					60	
Glu	Ser	Val	Gly	Asp	Thr	Ala	Ala	Ala	Asp	Ala	Val	Ala	Ala	Ala	
						65			70					75	
Gly	Leu	Pro	Ala	Asp	Ala	Val	Thr	Leu	Ala	Thr	Thr	Glu	Ala	Pro	Arg
						85			90					95	
Thr	Phe	Val	Asp	Val	Ile	Gly	Gly	Asn	Ala	Tyr	Tyr	Ile	Asn	Ala	Ser
						100			105					110	
Ser	Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Glu	Gly	Gly	Phe	Val	Thr	Ala
						115			120					125	
Gly	His	Cys	Gly	Arg	Ala	Gly	Ala	Ser	Thr	Ser	Ser	Pro	Ser	Gly	Thr
						130			135					140	
Phe	Arg	Gly	Ser	Ser	Phe	Pro	Gly	Asn	Asp	Tyr	Ala	Trp	Val	Gln	Val
						145			150					155	
Ala	Ser	Gly	Asn	Thr	Pro	Arg	Gly	Leu	Val	Asn	Asn	His	Ser	Gly	Gly
						165			170					175	
Thr	Val	Arg	Val	Thr	Gly	Ser	Gln	Gln	Ala	Ala	Val	Gly	Ser	Tyr	Val
						180			185					190	
Cys	Arg	Ser	Gly	Ser	Thr	Thr	Gly	Trp	Arg	Cys	Gly	Tyr	Val	Arg	Ala
						195			200					205	
Tyr	Asn	Thr	Thr	Val	Arg	Tyr	Ala	Glu	Gly	Ser	Val	Ser	Gly	Leu	Ile
						210			215					220	
Arg	Thr	Ser	Val	Cys	Ala	Glu	Pro	Gly	Asp	Ser	Gly	Gly	Ser	Leu	Val
						225			230					235	
Ala	Gly	Thr	Gln	Ala	Gln	Gly	Val	Thr	Ser	Gly	Gly	Ser	Gly	Asn	Cys
						245			250					255	

Arg Tyr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln  
 260 265 270  
 Ala Tyr Gly Leu Arg Leu Val Leu Gly His Ala Arg Gly Gly Pro Ser  
 275 280 285  
 Pro Ala Arg Arg Ala Pro Ala Pro Pro Ala Arg Ala  
 290 295 300

<210> 65  
 <211> 429  
 <212> DNA  
 <213> Cellulomonas xylinolytica

<400> 65  
 cgctgctcga tcgggttcgc cgtgacgggc ggcttcgtga ccggccggcca ctgcggacgg 60  
 tccggcgca cgacgacgtc gcccggcggc acgttcggccg ggtccagctt tcccccaac 120  
 gactacgcct gggtccgcgc ggcctcgggc aacacgccc tcggtgccgt gaaccgctac 180  
 gacggcagcc gggtggaccgt ggccgggtcc accgacgcgg ccgtcggtgc cgcggctgc 240  
 cggtcggggt cgacgaccgc gtggggctgc ggcacgatcc agtcccgcgg cgcgagcgtc 300  
 acgtacgccc agggcaccgt cagcgggctc atccgcacca acgtgtgcgc cgagccgggt 360  
 gactccgggg ggtcgctgat cgccggcacc caggcgcggg gcgtgacgta cggccggctcc 420  
 ggcaactgc 429

<210> 66  
 <211> 143  
 <212> PRT  
 <213> Cellulomonas xylinolytica

<400> 66

Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly  
 1 5 10 15  
 His Cys Gly Arg Ser Gly Ala Thr Thr Ser Pro Ser Gly Thr Phe  
 20 25 30  
 Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala  
 35 40 45  
 Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg  
 50 55 60  
 Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys  
 65 70 75 80  
 Arg Ser Gly Ser Thr Thr Ala Trp Gly Cys Gly Thr Ile Gln Ser Arg  
 85 90 95  
 Gly Ala Ser Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg  
 100 105 110  
 Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala  
 115 120 125  
 Gly Thr Gln Ala Arg Gly Val Thr Ser Gly Gly Ser Gly Asn Cys  
 130 135 140

<210> 67  
 <211> 1284  
 <212> DNA  
 <213> Oerskovia turbata

<400> 67  
 atggcacgat cattctggag gacgctcgcc acggcgtgcg ccgcgacggc actgggtgcc 60  
 ggcccccgcag cgctcacccgc gaaacgcccgcg acgcccaccc ccgacacccccc gaccgtttca 120  
 ccccagacct ctcgaaaggc ctcgcccgcg gtgctccgcg ccctccagcg ggacctgggg 180

ctgagcgcca	aggacgcgac	gaagcgtctg	gcgttccagt	ccgacgcggc	gagcaccgag	240
gacgcgtctcg	ccgacagcct	ggacgcctac	gcgggcgcct	gggtcgaccc	tgcgaggaac	300
accctgtacg	tcggcgtcgc	cgacagggcc	gaggccaagg	aggtccgttc	ggccggagcg	360
acccccgtgg	tcgtcgacca	cacgctcgcc	gagctcgaca	cgtggaaggc	ggcgctcgac	420
ggtgagctca	acgacccccgc	gggcgtcccc	agctggttcg	tcgacgtcac	gaccaccag	480
gtcgctgtca	acgtgcacga	cggcggacgc	gccctcgccg	agctggctgc	cgcgagcgcg	540
ggcgtgcccgc	ccgacgcccatt	cacctacgtg	acgacgaccg	aggctcctcg	tcccctcgtc	600
gacgtgggtgg	gcccgaacgc	gtacaccatg	ggttcggcgc	ggcgctgctc	ggtcggttc	660
gcggtgaacg	ggggcttcat	cacggccggg	cactgcggct	cggtcgccac	ccgcacctcg	720
ggggccggcgc	gcacgttccg	gggggtcgaac	ttccccggca	acgactacgc	ctgggtgcag	780
gtcgacgcgg	gtaacaccccc	ggtcggcgcg	gtcaacaact	acagcgggtgg	gcmcgtcgcg	840
gtcgccagggt	cgacggccgc	gcccgtgggg	gcctcggtct	gcccgtccgg	ttccacgacg	900
ggctggact	gcccgcacat	cggcgcgtac	aacacctcg	tgacgtaccc	gcagggcacc	960
gtctcggggc	tcatccgcac	gaacgtgtgc	gccgagcccg	gcgactcg	cggtcgctc	1020
ctcgccggca	accaggcgca	gggcgtgacc	tcgggcgggt	cgggcaactg	ctcgccggc	1080
gggacgacgt	acttccagcc	cgtcaacgag	gccctcg	ggtacgggt	cacgctcg	1140
acctctgacg	gtggggccccc	gagccgcgc	cgaccgggt	ccaggctat	gcgcggac	1200
accaggcgag	cgtctcg	gggacgtcgg	tcgcgcagcg	aacggttcgt	acgtcacgac	1260
cggggcg	cgaccgggt	tgcc				1284

<210> 68  
<211> 428  
<212> PRT  
<213> Oerskovia turbata

<400> 68

Met	Ala	Arg	Ser	Phe	Trp	Arg	Thr	Leu	Ala	Thr	Ala	Cys	Ala	Ala	Thr
1								5		10					15
Ala	Leu	Val	Ala	Gly	Pro	Ala	Ala	Leu	Thr	Ala	Asn	Ala	Ala	Thr	Pro
								20		25					30
Thr	Pro	Asp	Thr	Pro	Thr	Val	Ser	Pro	Gln	Thr	Ser	Ser	Lys	Val	Ser
								35		40					45
Pro	Glu	Val	Leu	Arg	Ala	Leu	Gln	Arg	Asp	Leu	Gly	Leu	Ser	Ala	Lys
							50		55		60				
Asp	Ala	Thr	Lys	Arg	Leu	Ala	Phe	Gln	Ser	Asp	Ala	Ala	Ser	Thr	Glu
							65		70		75				80
Asp	Ala	Leu	Ala	Asp	Ser	Leu	Asp	Ala	Tyr	Ala	Gly	Ala	Trp	Val	Asp
							85		90		95				
Pro	Ala	Arg	Asn	Thr	Leu	Tyr	Val	Gly	Val	Ala	Asp	Arg	Ala	Glu	Ala
							100		105		110				
Lys	Glu	Val	Arg	Ser	Ala	Gly	Ala	Thr	Pro	Val	Val	Val	Asp	His	Thr
							115		120		125				
Leu	Ala	Glu	Leu	Asp	Thr	Trp	Lys	Ala	Ala	Leu	Asp	Gly	Glu	Leu	Asn
							130		135		140				
Asp	Pro	Ala	Gly	Val	Pro	Ser	Trp	Phe	Val	Asp	Val	Thr	Thr	Asn	Gln
							145		150		155				160
Val	Val	Val	Asn	Val	His	Asp	Gly	Gly	Arg	Ala	Leu	Ala	Glu	Leu	Ala
							165		170		175				
Ala	Ala	Ser	Ala	Gly	Val	Pro	Ala	Asp	Ala	Ile	Thr	Tyr	Val	Thr	Thr
							180		185		190				
Thr	Glu	Ala	Pro	Arg	Pro	Leu	Val	Asp	Val	Val	Gly	Gly	Asn	Ala	Tyr
							195		200		205				
Thr	Met	Gly	Ser	Gly	Gly	Arg	Cys	Ser	Val	Gly	Phe	Ala	Val	Asn	Gly
							210		215		220				
Gly	Phe	Ile	Thr	Ala	Gly	His	Cys	Gly	Ser	Val	Gly	Thr	Arg	Thr	Ser
							225		230		235				240

Gly Pro Gly Gly Thr Phe Arg Gly Ser Asn Phe Pro Gly Asn Asp Tyr  
                  245                 250                 255  
 Ala Trp Val Gln Val Asp Ala Gly Asn Thr Pro Val Gly Ala Val Asn  
                  260                 265                 270  
 Asn Tyr Ser Gly Gly Arg Val Ala Val Ala Gly Ser Thr Ala Ala Pro  
                  275                 280                 285  
 Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys  
                  290                 295                 300  
 Gly Thr Ile Gly Ala Tyr Asn Thr Ser Val Thr Tyr Pro Gln Gly Thr  
                  305                 310                 315                 320  
 Val Ser Gly Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser  
                  325                 330                 335  
 Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly  
                  340                 345                 350  
 Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val  
                  355                 360                 365  
 Asn Glu Ala Leu Gly Gly Tyr Gly Leu Thr Leu Val Thr Ser Asp Gly  
                  370                 375                 380  
 Gly Gly Pro Ser Arg Arg Arg Pro Gly Ala Arg Ala Met Arg Gly Pro  
                  385                 390                 395                 400  
 Thr Arg Ala Ala Ser Arg Pro Gly Arg Arg Ser Arg Ser Glu Arg Phe  
                  405                 410                 415  
 Val Arg His Asp Arg Gly Arg Ala Thr Gly Cys Ala  
                  420                 425

<210> 69  
 <211> 524  
 <212> DNA  
 <213> Oerskovia jenensis

<400> 69  
 gccgctgctc ggtcggttc gcggtaacg gcggcttcgt caccgcaggc cactgcggga     60  
 cgggtggcac ccgcacctcg gggccggcgc gcacgttccg cgggtcgagc ttccccggca     120  
 acgactacgc ctgggtgcag gtcgacgcgg ggaacacccc ggtcggggcc gtcaacaact     180  
 acagcggtgg acgcgtcgcg gtcgcgggct cgacggccgc acccgtgggt tcctcggtct     240  
 gccggtccgg ttccacgacg ggctggcgct gcggcacat cgccgcctac aacagctcg     300  
 tgacgtaccc gcaggggacc gtctccgggc tcatccgcac caacgtgtgc gccgagccgg     360  
 gcgactcggg cggctcgctc ctcgcgggca accaggcaca gggcctgacg tcgggcgggt     420  
 cgggcaactg ctcgtcgggc ggcacgacgt acttccagcc cgtcaacgag gcgctctcg     480  
 cctacggcct cacgctcggt acctccggcg gcagggcaa ctgc     524

<210> 70  
 <211> 174  
 <212> PRT  
 <213> Oerskovia jenensis

<400> 70

Arg Cys Ser Val Gly Phe Ala Val Asn Gly Gly Phe Val Thr Ala Gly  
 1              5                 10                 15  
 His Cys Gly Thr Val Gly Thr Arg Thr Ser Gly Pro Gly Gly Thr Phe  
               20              25                 30  
 Arg Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Asp  
               35              40                 45  
 Ala Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Arg  
               50              55                 60  
 Val Ala Val Ala Gly Ser Thr Ala Ala Pro Val Gly Ser Ser Val Cys

65	70	75	80
Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile Ala Ala Tyr			
85	90	95	
Asn Ser Ser Val Thr Tyr Pro Gln Gly Thr Val Ser Gly Leu Ile Arg			
100	105	110	
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala			

115	120	125	
Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Ser			
130	135	140	
Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala Leu Ser Ala			
145	150	155	160
Tyr Gly Leu Thr Leu Val Thr Ser Gly Gly Arg Gly Asn Cys			
165	170		

<210> 71

<211> 984

<212> DNA

<213> Cellulosimicrobium cellulans

<400> 71

ccacgggcgg cgggtcgggc agcgcgctcg tcgggctcgc gggcaagtgc atcgacgtcc	60
ccgggtccga cttcagtgc acggcagcgc tccagctgtg gacgtgcaac gggtgcagg	120
cagcgcttggaa cggtcgaagc cgacggcacc gtacgcgcgg gcgcaagtgc catggacgtc	180
gcgtgggcgc cgcggccgac ggcacggcgc tccagctcgc gaactgcacg gcaacgcgc	240
ccagaagttc gtgctcaacg ggcggggcga cctcggtcgc gtgctggcga acaaagtgcg	300
tgcacgcgcg cgggtgcgcg ccggaggtact cgccgcgcg tacagagctca cggcgacgtg	360
cgcggcggcg accgctacat cacacgggac ccggggcgcgt cgtcggtcgc ggcctgctcg	420
atcgggtacg ccgtccaggc cggcttcgc acggcggggc actgcggacg cggcggaca	480
aggagagtgc tcaccgcgag ctgggcgcgc atggggacgg tccaggcggc gtcgttcccc	540
ggccacgact acgcgtgggt ggcgcgtcgc gcccggttct cccccgtccc gcgggtgaac	600
aactacgcgcg gcccgcaccgt cgacgtcgcg ggctcggccg aggcccgt gggtcgtcg	660
gtgtgcccgt cggcgcac gaccggctgg cgctcggcgc tcatcgagca gaagaacatc	720
accgtcaact acggcaacgg cgacgttccc ggcctcgtgc gggcagcgc gtgcggag	780
ggccggcact cggcgggtc ggtatctcc ggcaaccagg cgcaggcgt cacgtcgggc	840
aggatcaacg actgctcgaa cggcggcaag ttcccttacc agcccgatcg acggcctgtc	900
gctcgtgacc acggcggcggc ggtcggcag cgcgtcgtc gggctcgc gcaagtgcat	960
cgacgtcccc gggtccgact tcag	984

<210> 72

<211> 328

<212> PRT

<213> Cellulosimicrobium cellulans

<400> 72

Pro Arg Ala Ala Gly Arg Ala Ala Arg Ser Ser Gly Ser Arg Ala Ser			
1	5	10	15
Ala Ser Thr Ser Pro Gly Pro Thr Ser Val Thr Ala Ser Ala Ser Ser			
20	25	30	
Cys Gly Arg Ala Thr Gly Arg Arg Gln Arg Trp Thr Phe Glu Ala Asp			
35	40	45	
Gly Thr Val Arg Ala Gly Gly Lys Cys Met Asp Val Ala Trp Ala Pro			
50	55	60	
Arg Pro Thr Ala Arg Arg Ser Ser Arg Thr Ala Arg Gln Arg Gly			

65	70	75	80
Pro Glu Val Arg Ala Gln Arg Arg Gly Arg Pro Arg Val Gly Ala Gly			
85	90	95	
Glu Gln Ser Ala Ser Thr Pro Pro Gly Ala His Arg Gly Thr Arg Gly			
100	105	110	
Ala Val Arg Ala His Gly Asp Val Arg Gly Gly Asp Arg Tyr Ile Thr			
115	120	125	
Arg Asp Pro Gly Ala Ser Ser Gly Ser Ala Cys Ser Ile Gly Tyr Ala			
130	135	140	
Val Gln Gly Gly Phe Val Thr Ala Gly His Cys Gly Arg Gly Gly Thr			
145	150	155	160
Arg Arg Val Leu Thr Ala Ser Trp Ala Arg Met Gly Thr Val Gln Ala			
165	170	175	
Ala Ser Phe Pro Gly His Asp Tyr Ala Trp Val Arg Val Asp Ala Gly			
180	185	190	
Phe Ser Pro Val Pro Arg Val Asn Asn Tyr Ala Gly Gly Thr Val Asp			
195	200	205	
Val Ala Gly Ser Ala Glu Ala Pro Val Gly Ala Ser Val Cys Arg Ser			
210	215	220	
Gly Ala Thr Thr Gly Trp Arg Cys Gly Val Ile Glu Gln Lys Asn Ile			
225	230	235	240
Thr Val Asn Tyr Gly Asn Gly Asp Val Pro Gly Leu Val Arg Gly Ser			
245	250	255	
Ala Cys Ala Glu Gly Gly Asp Ser Gly Gly Ser Val Ile Ser Gly Asn			
260	265	270	
Gln Ala Gln Gly Val Thr Ser Gly Arg Ile Asn Asp Cys Ser Asn Gly			
275	280	285	
Gly Lys Phe Leu Tyr Gln Pro Asp Arg Arg Pro Val Ala Arg Asp His			
290	295	300	
Gly Arg Arg Val Gly Gln Arg Ala Arg Arg Ala Arg Gly Gln Val His			
305	310	315	320
Arg Arg Pro Arg Val Arg Leu Gln			
325			

<210> 73

<211> 257

<212> DNA

<213> Promicromonospora citrea

<400> 73

ttccccggca acgactacgc gtgggtgaac acgggcacgg acgacaccct cgtcgccgccc	60
gtgaacaact acagcggcgg cacggtaac gtcggggct cgaccgtgc cgccgtcgcc	120
gcgacggtct gccgctcggt ctccacgacc ggctggcact gcggcaccat ccaggcgctg	180
aacgcgtcgg tcacctacgc cgagggcacc gtgagcggcc tcatccgcac caacgtgtgc	240
gccgagcccg gcgactc	257

<210> 74

<211> 85

<212> PRT

<213> Promicromonospora citrea

<400> 74

Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Thr Gly Thr Asp Asp Thr			
1	5	10	15
Leu Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala			
20	25	30	

Gly Ser Thr Arg Ala Ala Val Gly Ala Thr Val Cys Arg Ser Gly Ser  
   35                          40                          45  
 Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Leu Asn Ala Ser Val  
   50                          55                          60  
 Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys  
   65                          70                          75                          80  
 Ala Glu Pro Gly Asp  
   85

<210> 75  
 <211> 257  
 <212> DNA  
 <213> Promicromonospora sukumoe

<400> 75  
 ttccccggca acgactacgc gtgggtgaac gtcggctccg acgacacccc gatcggtgcg         60  
 gtcaacaact acagcggcgg caccgtgaac gtcgcggct cgacccaggc cgccgtcggc         120  
 tccaccgtct gccgctccgg ttccacgacc ggctggcaact gcggcaccat ccaggccttc         180  
 aacgcgtcgg tcacctacgc cgagggcacc gtgtccggcc tgatccgcac caacgtctgc         240  
 gccgagcccg gcgactc   257

<210> 76  
 <211> 85  
 <212> PRT  
 <213> Promicromonospora sukumoe

<400> 76

Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Val Gly Ser Asp Asp Thr  
 1                          5                          10                          15  
 Pro Ile Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala  
   20                          25                          30  
 Gly Ser Thr Gln Ala Ala Val Gly Ser Thr Val Cys Arg Ser Gly Ser  
   35                          40                          45  
 Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Phe Asn Ala Ser Val  
   50                          55                          60  
 Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys  
   65                          70                          75                          80  
 Ala Glu Pro Gly Asp  
   85

<210> 77  
 <211> 430  
 <212> DNA  
 <213> Xylanibacterium ulmi

<400> 77  
 gccgctgctc gatcggttgc gccgtgacgg gcggcttcgt gaccgccggc cactcggtac         60  
 ggtccggcgc gacgacgacg tccgcgagcg gcacgttcgc cgggtccagc tttccggca         120  
 acgactacgc ctgggtccgc gcggcctcgga acacacgccc gtcggtgccg tgaaccgcta         180  
 cgacggcagc cgggtgaccg tggccgggtc caccgacgccc gccgtcggtg ccggcggtctg         240  
 ccggtcgggg tcgacgaccg cgtggcgctg cggcacgatc cagtcccgcc ggcgcgacgg         300  
 cacgtacgccc cagggcaccg tcagcggtc catccgcacc aacgtgtccg cggagccgg         360  
 tgactccggg gggtcgctga tcgcggcac ccaggcgcag ggcgtgacgt ccggcggtctc         420  
 cggcaactgc   430

<210> 78

<211> 141  
<212> PRT  
<213> Xylanibacterium ulmi

<400> 78

Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly  
1 5 10 15  
His Cys Gly Arg Ser Gly Ala Thr Thr Ser Ala Ser Gly Thr Phe  
20 25 30  
Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala  
35 40 45  
Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg  
50 55 60  
Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys  
65 70 75 80  
Arg Ser Gly Ser Thr Thr Ala Trp Arg Cys Gly Thr Ile Gln Ser Arg  
85 90 95  
Gly Ala Thr Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg  
100 105 110  
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala  
115 120 125  
Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly  
130 135 140

<210> 79

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 79  
acccacgcgt agtcgttgcc

20

<210> 80  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 80  
acccacgcgt agtcgtkgcc gggg

24

<210> 81  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 81

tcgtcggtt cgccgg	18
<210> 82	
<211> 17	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 82	
cgacgtgctc ggcggc	17
<210> 83	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 83	
cgcgccagc tcgcggtg	18
<210> 84	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 84	
cggccccgag gtgcgggtgc cg	22
<210> 85	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 85	
cagcgtctcc ggcctcatcc gc	22
<210> 86	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 86	
ctcggtctcg ggcctcatcc gc	22

<210> 87	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 87	
cgacgttccc ggcctcgtgc gc	22
<210> 88	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 88	
caccgtctcg gggctcatcc gc	22
<210> 89	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 89	
agcarcgtgt gcgccgagcc	20
<210> 90	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 90	
ggcagcgcgt gcgccggagg	20
<210> 91	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 91	
gccgctgctc gatcgggttc	20
<210> 92	
<211> 24	

<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 92  
gcagttgccg gagccggccgg acgt 24

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 93  
tgcgccgagc ccggcgactc cggc 24

<210> 94  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 94  
ggcacgacgt acttccagcc cgtgaac 27

<210> 95  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 95  
gaccacacgacg tagtcgttgc cggggAACGA cga 33

<210> 96  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 96  
gaagggtcccc gacggtgacg acgtgctcgc gcc 33

<210> 97  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 97  
caggcgagg gcgtgacctc gggcggtcg 30

<210> 98  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 98  
ggcgggacga cgtacttcca gcccgtaaa 29

<210> 99  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 99  
cacccacgca tagtcgtggc cggggAACGA 30

<210> 100  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 100  
gaagccgccc tggacggcgt acccgatcga gca 33

<210> 101  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 101  
tgcgcgagg gcggcgactc gggcggtcg 30

<210> 102  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 102  
ttcctctacc agccgtcaa cccgatccta 30

<210> 103  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 103  
cgccgcgggg acgaacccgc cctcgaccgc gaa 33

<210> 104  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 104  
cgcgtagtcg ttgccgggga acgacgagcc 30

<210> 105  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 105  
ggcctcatcc gcacgagcgt gtgcgccgag 30

<210> 106  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 106  
acgtcggcgt ggtccggcaa ctgccgtac gggggc 36

<210> 107  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 107  
gagcccgta caccggaggg cctcggtgac gggctggaa 39

<210> 108  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 108  
cgtcacgccc tgcgcctggc tgcccgcgag 30

<210> 109  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 109  
tccagccgt caacgaggcc ctccgggtgt acgggctc 38

<210> 110  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 110  
acgtcggtcg cgcaaggaa cggttcgta gtc 33

<210> 111  
<211> 30

<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 111  
cgtggtcgca ccggtcgtgc cgcagtgc 30

<210> 112  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 112  
gacgacgacc gtgttggtag tgacgtcgac gtacca 36

<210> 113  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 113  
tccaccacgg ggtggcgctg cgggacgatc 30

<210> 114  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 114  
gtgtgcgcgg agcccgccga ctccggcgcc 30

<210> 115  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 115  
gctcggggccc ccaccgtcag aggtcacgag cgtgag 36

<210> 116  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 116  
atggcacgat cattctggag gacgctcgcc acggcg 36

<210> 117  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 117  
tgctcgatcg ggtacgcccgt ccagggcgcc ttc 33

<210> 118  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 118  
taggatcggtttagacggct ggttagaggaa 30

<210> 119  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 119  
tggtacgtcg acgtcaactac caacacggtc gtcgtc 36

<210> 120  
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<220>  
<223> primer

<400> 120  
gccgcggag tcgccccggct cggcgcacac 30

<210> 121  
<211> 30  
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<220>  
<223> primer

<400> 121  
gtsgacgtsa tcggsggsaa cgcttactac 30

<210> 122  
<211> 18  
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<220>  
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<220>  
<221> misc\_feature  
<222> (13)..(16)  
<223> n is a, c, g, or t

<400> 122  
sgcsgtsgcs ggnganga 18

<210> 123  
<211> 27  
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<213> Artificial Sequence

<220>  
<223> primer

<400> 123  
gtsgaygtsa tcggcggcga ygcstac 27

<210> 124  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<220>  
<221> misc\_feature  
<222> (10)..(16)  
<223> n is a, c, g, or t

<400> 124  
sgasgcgtan ccctgncc 18

<210> 125  
<211> 189  
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<220>  
<223> consensus sequence

<220>  
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93, 109-111, 113, 116, 159, 160, 163-166, 169-189  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> 4, 19, 28, 108, 126  
<223> Xaa is Ile or Val

<220>  
<221> VARIANT  
<222> 7, 157  
<223> Xaa is Asn or Asp

<220>

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<222> 92, 99, 143  
<223> Xaa is Ser or Ala

<220>  
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<222> 112, 156  
<223> Xaa is Asn or Gly

<220>  
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<222> 21  
<223> Xaa is Phe or Tyr

<220>  
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<222> 40  
<223> Xaa is Thr or Val

<220>  
<221> VARIANT  
<222> 59  
<223> Xaa is Phe or Trp

<220>  
<221> VARIANT  
<222> 65  
<223> Xaa is Gly or Asp

<220>  
<221> VARIANT  
<222> 68  
<223> Xaa is Leu or Phe

<220>  
<221> VARIANT  
<222> 74  
<223> Xaa is Asn or Arg

<220>  
<221> VARIANT  
<222> 75  
<223> Xaa is Tyr or His

<220>  
<221> VARIANT  
<222> 76  
<223> Xaa is Ser or Asp

<220>  
<221> VARIANT  
<222> 78  
<223> Xaa is Gly or Ser

<220>  
<221> VARIANT  
<222> 79

<223> Xaa is Arg or Thr

<220>

<221> VARIANT

<222> 83

<223> Xaa is Ala or Thr

<220>

<221> VARIANT

<222> 85

<223> Xaa is His or Ser

<220>

<221> VARIANT

<222> 86

<223> Xaa is Thr or Gln

<220>

<221> VARIANT

<222> 102

<223> Xaa is Gly or Ala

<220>

<221> VARIANT

<222> 104

<223> Xaa is His or Arg

<220>

<221> VARIANT

<222> 107

<223> Xaa is Thr or Tyr

<220>

<221> VARIANT

<222> 114

<223> Xaa is Ser or Thr

<220>

<221> VARIANT

<222> 118

<223> Xaa is Pro or Ala

<220>

<221> VARIANT

<222> 119

<223> Xaa is Glu or Gln

<220>

<221> VARIANT

<222> 121

<223> Xaa is Thr, Ser, or Asp

<220>

<221> VARIANT

<222> 123

<223> Xaa is Arg or Ser

<220>  
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<223> Xaa is Thr or Gly

<220>  
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<223> Xaa is Thr, Asn, or Ser

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<223> Xaa is Val or Ala

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<223> Xaa is Pro or Gly

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<223> Xaa is Leu or Val

<220>  
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<222> 142  
<223> Xaa is Leu, Val, or Ile

<220>  
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<222> 145  
<223> Xaa is Asn or Thr

<220>  
<221> VARIANT  
<222> 148  
<223> Xaa is Gln or Arg

<220>  
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<222> 150  
<223> Xaa is Val or Leu

<220>  
<221> VARIANT  
<222> 154  
<223> Xaa is Gly or Arg

<220>  
<221> VARIANT  
<222> 155  
<223> Xaa is Ser or Ile

<400> 125

Xaa Asp Val Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15  
Cys Ser Xaa Gly Xaa Ala Val Xaa Gly Gly Phe Xaa Thr Ala Gly His  
20 25 30  
Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Thr Phe Xaa  
35 40 45  
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Xaa Val Xaa Xaa Xaa Xaa  
50 55 60  
Xaa Xaa Xaa Xaa Xaa Xaa Val Asn Xaa Xaa Xaa Gly Xaa Xaa Val  
65 70 75 80  
Xaa Val Xaa Gly Xaa Xaa Xaa Ala Xaa Val Gly Xaa Xaa Val Cys Arg  
85 90 95  
Ser Gly Xaa Thr Thr Xaa Trp Xaa Cys Gly Xaa Xaa Xaa Xaa Xaa Xaa  
100 105 110  
Xaa Xaa Val Xaa Tyr Xaa Xaa Gly Xaa Val Xaa Gly Leu Xaa Arg Xaa  
115 120 125  
Xaa Xaa Cys Ala Glu Xaa Gly Asp Ser Gly Ser Xaa Xaa Xaa Gly  
130 135 140  
Xaa Gln Ala Xaa Gly Xaa Thr Ser Gly Xaa Xaa Xaa Xaa Cys Xaa Xaa  
145 150 155 160  
Gly Gly Xaa Xaa Xaa Xaa Gln Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
165 170 175  
Xaa  
180 185

<210> 126  
<211> 16  
<212> PRT  
<213> Cellulomonas cellasea

<220>  
<221> VARIANT  
<222> (1)..(1)  
<223> Xaa is Ile or Tyr

<400> 126

Xaa Ala Trp Asp Ala Phe Ala Glu Asn Val Val Asp Trp Ser Ser Arg  
1 5 10 15

<210> 127  
<211> 17  
<212> PRT  
<213> Cellulomonas cellasea

<400> 127

Tyr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln Ala  
1 5 10 15  
Tyr

<210> 128  
<211> 11  
<212> PRT  
<213> Cellulomonas flavigena

<220>  
<221> VARIANT  
<222> (4)..(11)  
<223> Xaa is Ile or Tyr

<400> 128

Val Asp Val Xaa Gly Gly Asn Ala Tyr Tyr Xaa  
1 5 10

<210> 129  
<211> 9  
<212> PRT  
<213> Cellulomonas fimi

<220>  
<221> VARIANT  
<222> (4)..(4)  
<223> Xaa is Ile or Tyr

<400> 129

Val Asp Val Xaa Gly Gly Asp Ala Tyr  
1 5

<210> 130  
<211> 305  
<212> DNA  
<213> Aspergillus niger

<220>  
<221> misc\_feature  
<222> (186)..(186)  
<223> n is a, c, g, or t

<400> 130

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aactgctcac	cctcggttgt	ggtgacctgg	aggtaaagca	agtgaccctt	ctggcggagg	120
tggtaaggaa	cgggggttcca	cggggagaga	gagatggcct	tgacggcttt	gggaagggga	180
gcttcngcgc	gggggaggat	ggtcttgaga	gagggggagc	tagtaatgtc	gtacttggac	240
aggagtgct	ccttctccga	cgcattcagcc	acctcagcgg	agatggcatc	gtgcagagac	300
agacc						305

<210> 131  
<211> 1488  
<212> DNA  
<213> Cellulomonas strain 69B4

<400> 131

atgacaccac	gaactgtcac	aagagctctg	gctgtggcaa	cagcagctgc	tacactcttg	60
gctggggta	tggcagcaca	agctaacgaa	ccggctcctc	caggatctgc	atcagcccct	120
ccacgattag	ctgaaaaact	tgaccctgac	ttacttgaag	caatggAACG	cgatctgggg	180
ttagatgcag	aggaagcagc	tgcaacgtta	gctttcagc	atgacgcagc	tgaaacggga	240
gaggctctt	ctgaggaact	cgacgaagat	ttcgccggca	cgtgggttga	agatgtatgt	300
ctgtatgtt	caaccactga	tgaagatgtc	gttgaagaag	tgcaggcga	aggagcaact	360
gctgtgactg	ttgagcattc	tcttgctgt	ttagaggcgt	ggaagacgt	tttgatgtct	420
gcgtggagg	gtcatgtga	tgtgcctacg	ttgtacgtcg	acgtgcctac	gaattcggta	480

gtcgttgctg	taaaggcagg	agcgcaggat	gtagctgcag	gacttgtgga	aggcgctgat	540
gtgccatcac	atgcggtcac	ttttagaa	acggacgaaa	cgcctagaac	gatgttcgac	600
gtaattggag	gcaacgcata	tactattggc	ggccggctca	gatgttctat	cgattcgca	660
gtaaacggtg	gcttcattac	tgccggtcac	tgcgaaagaa	caggagccac	tactgccaat	720
ccgactggca	cattgcagg	tagctcgtt	ccggaaaatg	attatgcatt	cgtccgaaca	780
ggggcaggag	taaatttgct	tgcccaagtc	aataactact	cgggcggcag	agtccaagta	840
gcaggacata	cggccgcacc	agttggatct	gctgtatgcc	gctcaggtag	cactacaggt	900
tggcattgct	gaactatcac	ggcgctgaat	tcgtctgtca	cgtatccaga	ggAACAGTC	960
cgaggactta	tccgcacgac	ggttgtgcc	gaaccaggta	atagcggagg	tagccttta	1020
gcggaaatc	aagcccagg	tgtcacgtca	ggtgggtctg	gaaattgtcg	gacggggggga	1080
acaacattct	ttcaaccagt	caacccgatt	ttgcaggctt	acggcctgag	aatgattacg	1140
actgactctg	gaagttcccc	tgctccagca	cctacatcat	gtacaggcta	cgcaagaacg	1200
ttcacaggaa	ccctcgccgc	aggaagagca	gcagctcaac	cgaacggtag	ctatgttcag	1260
gtcaaccgga	gcggtacaca	ttccgtctgt	ctcaatggac	ctagcggtag	ggactttgat	1320
ttgtatgtgc	agcgatggaa	tggcagtagc	tggtaaccg	tcgctcaatc	gacatcgccg	1380
ggaagcaatg	aaaccattac	gtaccgcgg	aatgtggat	attatgcata	cgtggtaac	1440
gctcggtcag	gatcaggagc	ttacacaatg	ggactcaccc	tcccctga		1488

<210> 132  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> linker

<400> 132

Asp	Asp	Asn	Asp	Pro	Ile
1			5		

<210> 133  
<211> 1020  
<212> DNA  
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<220>  
<223> synthetic

<400> 133						
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ctaagtatta	gtaacgtga	attagtcaat	gaacgaggcg	aacaagttca	gttaaaaggg	180
atgagttccc	atggttcgca	atggtacggt	caatttgtaa	actatgaaag	catgaaatgg	240
ctaagagatg	attggggaaat	aactgtattc	cgagcagcaa	tgtataccctc	ttcaggagga	300
tatattgacg	atccatcagt	aaaggaaaaa	gtaaaagaga	ctgttgaggc	tgcgatagac	360
cttggcataat	atgtgatcat	tgattggcat	atcccttcag	acaatgaccc	aatatatat	420
aaagaagaag	cgaaggattt	cttgcataaa	atgtcagagt	tgtatggaga	ctatccgaat	480
gtgatatacg	aaattgcaaa	tgaaccgaat	ggtgtgtat	ttacgtggaa	caatcaaata	540
aaaccgtatg	cagaagaat	gattccggtt	attcgtgaca	atgaccctaa	taacattgtt	600
attgttaggtt	caggtacatg	gagtcaggat	gtccatcatg	cagccgataa	tcatgttgc	660
gatcctaacg	tcatgtatgc	atttcatttt	tatgcaggaa	cacatggaca	aaatttacga	720
gaccaagtag	attatgcatt	agatcaagga	gcagcgat	ttgttagtga	atggggaca	780
agtgcagcta	caggtgatgg	tggtgtgttt	ttagatgaag	cacaagtgtg	gattgactt	840
atggatgaaa	gaaatttaag	ctgggccaac	tggctctaa	cgcataagga	tgagtcatct	900
gcagcgtaa	tgccaggtgc	aaatccaact	ggtgggtgga	cagaggctga	actatctcca	960
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<210> 134  
<211> 340  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic

<400> 134

Val Arg Ser Lys Lys Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu  
1 5 10 15  
Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Asp Asp Tyr  
20 25 30  
Ser Val Val Glu Glu His Gly Gln Leu Ser Ile Ser Asn Gly Glu Leu  
35 40 45  
Val Asn Glu Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His

50 55 60  
Gly Leu Gln Trp Tyr Gly Gln Phe Val Asn Tyr Glu Ser Met Lys Trp  
65 70 75 80  
Leu Arg Asp Asp Trp Gly Ile Thr Val Phe Arg Ala Ala Met Tyr Thr  
85 90 95  
Ser Ser Gly Gly Tyr Ile Asp Asp Pro Ser Val Lys Glu Lys Val Lys  
100 105 110  
Glu Thr Val Glu Ala Ala Ile Asp Leu Gly Ile Tyr Val Ile Ile Asp  
115 120 125  
Trp His Ile Leu Ser Asp Asn Asp Pro Asn Ile Tyr Lys Glu Glu Ala  
130 135 140  
Lys Asp Phe Phe Asp Glu Met Ser Glu Leu Tyr Gly Asp Tyr Pro Asn  
145 150 155 160  
Val Ile Tyr Glu Ile Ala Asn Glu Pro Asn Gly Ser Asp Val Thr Trp  
165 170 175  
Asp Asn Gln Ile Lys Pro Tyr Ala Glu Glu Val Ile Pro Val Ile Arg  
180 185 190  
Asp Asn Asp Pro Asn Asn Ile Val Ile Val Gly Thr Gly Thr Trp Ser  
195 200 205  
Gln Asp Val His His Ala Ala Asp Asn Gln Leu Ala Asp Pro Asn Val  
210 215 220  
Met Tyr Ala Phe His Phe Tyr Ala Gly Thr His Gly Gln Asn Leu Arg  
225 230 235 240  
Asp Gln Val Asp Tyr Ala Leu Asp Gln Gly Ala Ala Ile Phe Val Ser  
245 250 255  
Glu Trp Gly Thr Ser Ala Ala Thr Gly Asp Gly Gly Val Phe Leu Asp  
260 265 270  
Glu Ala Gln Val Trp Ile Asp Phe Met Asp Glu Arg Asn Leu Ser Trp  
275 280 285  
Ala Asn Trp Ser Leu Thr His Lys Asp Glu Ser Ser Ala Ala Leu Met  
290 295 300  
Pro Gly Ala Asn Pro Thr Gly Gly Trp Thr Glu Ala Glu Leu Ser Pro  
305 310 315 320  
Ser Gly Thr Phe Val Arg Glu Lys Ile Arg Glu Ser Ala Ser Asp Asn  
325 330 335  
Asn Asp Pro Ile  
340

<210> 135  
<211> 30  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 135

Met Arg Ser Lys Lys Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr  
1 5 10 15  
Ala Ala Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala  
20 25 30

<210> 136  
<211> 30  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 136

Met Arg Ser Lys Lys Leu Trp Ile Ser Leu Leu Leu Ala Val Ala Thr  
1 5 10 15  
Ala Ala Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala  
20 25 30

<210> 137  
<211> 40  
<212> DNA  
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<220>  
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<400> 137  
ctagctaggt accatgacac cacgaactgt cacaagagct

40

<210> 138  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 138  
gtgtgcaagg tttcagggga gggtgagtcc catttgtaa

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<210> 139  
<211> 40  
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<220>  
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<400> 139  
ctagctaggt accatgacac cacgaactgt cacaagagct

40

<210> 140  
<211> 37  
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<400> 140  
gtgtgcaagc tttcaagggg aacttccaga gtcagtc 37

<210> 141  
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<212> DNA  
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<400> 141  
tcatgcaggg taccatgaga agcaagaagc gaactgtcac aagagctctg gct 53

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gtgtgcaagc tttcagggga gggtgagtcc cattgtgtaa 40

<210> 143  
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<400> 143  
tcatgcaggg taccatgaga agcaagaagc gaactgtcac aagagctctg gct 53

<210> 144  
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gtgtgcaagc tttcaagggg aacttccaga gtcagtc 37

<210> 145

<211> 74  
<212> DNA  
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<220>  
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cagcagctgc taca 74

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gtgtgcaagc ttccagggg aggtgagtcc cattgtgtaa 40

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cagcagctgc taca 74

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gtgtgcaagc ttcaagggg aacttccaga gtcagtc 37

<210> 149  
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ccataccgga tccaaacgaa ccggctcctc caggatct 38  
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<400> 150  
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<211> 48  
<212> DNA  
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<400> 151  
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<400> 152  
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<210> 153  
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<400> 153  
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<210> 154  
<211> 38  
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<220>  
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<400> 154  
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<210> 155  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 155  
tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag 45

<210> 156  
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<220>  
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<400> 156  
cgtacatccc gggtcagggg agggtgagtc ccattg 36

<210> 157  
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tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag 45

<210> 158  
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<210> 161  
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ttagctgcta gcaaaaggag agggtaaaga atgagaagca agaag 45

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catgcattccc gggtaaggg gaacttccag agtcagtc 38

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tgcagtctgc tagcaaaagg agaggtaaaa gagtgagaag 40

<210> 164  
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<210> 165  
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<400> 165  
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<210> 166  
<211> 42  
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<220>  
<223> primer

<400> 166  
taaagagtga gaagaaaaaa acgcacagtc acgcgggccc tg 42

<210> 167  
<211> 35  
<212> DNA  
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<220>  
<223> primer

<400> 167  
gtcctctgtt aacttacggg ctgctgcccg agtcc 35

<210> 168  
<211> 41  
<212> DNA

<213> Artificial Sequence

<220>  
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<400> 168  
gcaacatgtc tgcgaggct aacgaaccgg ctcctccagg a 41

<210> 169  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 169  
gacatgacat aagcttaagg ggaacttcca gagtc 35

<210>	170					
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gagccgaatt	catataacctg	ccgtt	25			
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tcctggagga	gccggttcgt	tagcctgcgc	agacatgttg	c		
 <210>	172					
<211>	5713					
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Pro

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35 40 45	
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50 55 60	
Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu	
65 70 75 80	
Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr	
85 90 95	

Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala  
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           130                 135                 140  
 Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn  
           145                 150                 155                 160  
 Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly  
           165                 170                 175  
 Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu  
           180                 185                 190  
 Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala  
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 Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn  
           210                 215                 220  
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           245                 250                 255  
 Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val  
           260                 265                 270  
 Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala  
           275                 280                 285  
 Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His  
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           340                 345                 350  
 Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro  
           355                 360                 365  
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cattctcagg ccgtaagcsn ncaaaaatcggttgactgg 39

<210> 580  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<220>  
<221> misc\_feature  
<222> (20)..(21)  
<223> n is a, c, g, or t

<400> 580  
aatcattctc aggccgtasn nctgaaaaat cgggttgac 39

<210> 581  
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<220>  
<223> primer

<220>  
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<223> n is a, c, g, or t

<400> 581  
cgtaatcatt ctcaggccsn nagcctgcaa aatcgggtt 39

<210> 582  
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<220>  
<223> primer

<220>  
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<223> n is a, c, g, or t

<400> 582  
agtgcgtatc attctcagsn ngtaagcctg caaaaatcggttgactgg 39

<210> 583  
<211> 39

<212> DNA  
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<220>  
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<220>

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<223> n is a, c, g, or t

<400> 583  
gtcagtcgta atcattctsn ngccgtaagc ctgcaaaat 39

<210> 584  
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<220>  
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<220>

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<223> n is a, c, g, or t

<400> 584  
agagtca gtaatcatsn ncaggccgta agcctgcaa 39

<210> 585

<211> 39  
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<220>  
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<220>

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<223> n is a, c, g, or t

<400> 585  
tccagagtca gtcgtaatsn ntctcaggcc gtaaggctg 39

<210> 586  
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<220>  
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<220>

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<400> 586  
acttccagag tcagtcgtsn ncattctcag gccgttaagc 39

<210> 587  
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<220>  
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<400> 587  
ggaacttcca gagtcagtsn naatcattct caggccgta 39

<210> 588  
<211> 39  
<212> DNA  
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<220>  
<223> primer

<220>  
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<223> n is a, c, g, or t

<400> 588  
aggggaactt ccagagtcgn ncgtaatcat tctcaggcc 39

<210> 589  
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<212> DNA  
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<220>  
<223> primer

<220>  
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<223> n is a, c, g, or t

<400> 589  
ttaagggaa cttccagasn nagtcgtaat cattctcag 39

<210> 590  
<211> 39

<212> DNA  
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<220>  
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<220>  
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<222> (20)..(21)  
<223> n is a, c, g, or t

<400> 590  
gggttaaggg gaacttccsn ngtcagtcgt aatcattct 39

<210> 591  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<220>  
<221> misc\_feature  
<222> (20)..(21)  
<223> n is a, c, g, or t

<400> 591  
gttgggttaa ggggaactsn nagagtcagt cgtaatcat 39

<210> 592  
<211> 39  
<212> DNA  
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<220>  
<223> primer

<220>  
<221> misc\_feature  
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<400> 592  
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<210> 593  
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<220>  
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<220>

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<400> 593  
tcctctgttg ggttaaggsn nacttccaga gtcagtcgt 39

<210> 594  
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<212> DNA  
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<220>  
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<220>  
<221> misc\_feature  
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<223> n is a, c, g, or t

<400> 594  
ccgtcctctg ttgggttasn nggaacttcc agagtcagt 39

<210> 595  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 595  
gcataatacta ttggcggcct gtctagatgt tctatcgga 39

<210> 596  
<211> 38  
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<220>  
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<400> 596  
actattggcg gccggctca gtgttctatc ggattcgc 38

<210> 597  
<211> 37  
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<220>  
<223> primer

<400> 597  
ctgccggctca ctgcggattt acaggagcca ctactgc 37

<210> 598

<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 598  
atgattatgc attcgctca acagggcag gagtaaat 38

<210> 599  
<211> 40  
<212> DNA  
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<220>  
<223> primer

<400> 599  
ataactactc gggcgccaca gtccaagtag caggacatac 40

<210> 600  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 600  
atccagaggg aacagtcttg ggacttatcc gcacgac 37

<210> 601  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 601  
cagtccgagg acttatccag acgacggttt gtgccgaac 39

<210> 602  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 602  
gtggttctgg aaattgtcag acgggggaa caacattc 38

<210> 603

<211> 37  
<212> DNA  
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<220>  
<223> primer

<400> 603  
tgcaggctta cggcctgcag atgattacga ctgactc 37

<210> 604  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 604  
ttggcgcccg gtctagatca tctatcgat tcgcagta 38

<210> 605  
<211> 38  
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<220>  
<223> primer

<400> 605  
tcattactgc cggtcaactca ggaagaacag gagccact 38

<210> 606  
<211> 37  
<212> DNA  
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<220>  
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<400> 606  
cagttggatc tgctgtatct cgctcaggta gcactac 37

<210> 607  
<211> 37  
<212> DNA  
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<220>  
<223> primer

<400> 607  
cactacaggt tggcattcag gaactatcac ggcgctg 37

<210> 608  
<211> 38  
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<213> Artificial Sequence

<220>

<223> primer

<400> 608  
cttatccgca cgacggttc agccgaacca ggtgatag 38

<210> 609

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 609  
caggtggttc tggaaattca cggacggggg gaacaac 37

<210> 610

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 610  
tgcctcacat ttgtgccac 19

<210> 611

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 611  
caggatgtag ctgcaggac 19

<210> 612

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 612  
ctcggttatg agttagttc 19

<210> 613

<211> 50

<212> DNA

<213> Artificial Sequence

<220>  
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<400> 613  
cagagacaga ccccccggagg taaccatggc acgatcattc tggaggacgc 50

<210> 614  
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<212> DNA  
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<220>  
<223> primer

<400> 614  
gcgtcctcca gaatgatcggt cccatgggta cctccggggg tctgtctctg 50

<210> 615  
<211> 55  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 615  
atccgctcgc ggatccccat tgcagctcg ggcccccacc gtcagaggc acgag 55

<210> 616  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 616  
gcagcctgaa ctatggcga tcctctagag atcgaacttc at 42

<210> 617  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 617  
agaccgacga gaccccgccg accatggtcg acgtcatcg cgcaacgcg tactac 56

<210> 618  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 618  
tcagccgatc cgctcgcgga tccccattgt cagcccagga cgagacgcag accgta 56

<210> 619  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 619  
gttagtacgctg ttgccggccga tgacgtcgac catggtccgc ggggtctcggt cggctct 56

<210> 620  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 620  
gcagcctgaa ctatgtcgat tcctcttagat atcgaacttc atgttcga 48

<210> 621  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 621  
accgacgaga ccccgccggac catgcacggc gacgtgcgcg gcggcgaccg cta 53

<210> 622  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 622  
tagcggtcgac cgccgcgcac gtcgcccgtgc atggtccgcg ggggtctcggtc ggt 53

<210> 623  
<211> 59  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 623

tcagccgatc cgctcgccga tccccattgt cagcgagccc gacgagcgcg ctgccccac

59

<210> 624

<211> 184

<212> PRT

<213> Cellulomonas strain 69B4

<400> 624

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg  
1 5 10 15  
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His  
20 25 30  
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala  
35 40 45  
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala  
50 55 60  
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val  
65 70 75 80  
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg  
85 90 95  
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn  
100 105 110  
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr  
115 120 125  
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly  
130 135 140  
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr  
145 150 155 160  
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr  
165 170 175  
Gly Leu Arg Met Ile Thr Thr Asp  
180

<210> 625

<211> 187

<212> PRT

<213> Streptomyces griseus

<400> 625

Val Leu Gly Gly Ala Ile Tyr Gly Gly Ser Arg Cys Ser Ala  
1 5 10 15  
Ala Phe Asn Val Thr Lys Gly Gly Ala Arg Tyr Phe Val Thr Ala Gly  
20 25 30  
His Cys Thr Asn Ile Ser Ala Asn Trp Ser Ala Ser Ser Gly Gly Ser  
35 40 45  
Val Val Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn Asp Tyr Gly  
50 55 60  
Ile Val Arg Tyr Thr Asp Gly Ser Ser Pro Ala Gly Thr Val Asp Leu  
65 70 75 80  
Tyr Asn Gly Ser Thr Gln Asp Ile Ser Ser Ala Ala Asn Ala Val Val  
85 90 95  
Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly  
100 105 110  
Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val  
115 120 125

Tyr Asn Met Val Arg Thr Thr Ala Cys Ser Ala Gly Gly Asp Ser Gly  
130 135 140  
Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His Ser Gly Ser  
145 150 155 160  
Ser Gly Cys Ser Gly Thr Ala Gly Ser Ala Ile His Gln Pro Val Thr  
165 170 175  
Glu Ala Leu Ser Ala Tyr Gly Val Thr Val Tyr  
180 185

<210> 626

<211> 185

<212> PRT

<213> Streptomyces griseus

<400> 626

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu  
1 5 10 15  
Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly  
20 25 30  
His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser Ala Arg Thr  
35 40 45  
Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn Asn Asp Tyr  
50 55 60  
Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp Gly Thr Val  
65 70 75 80  
Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly Met Ala  
85 90 95  
Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly Ser Val Thr  
100 105 110  
Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val Val Tyr Gly  
115 120 125

Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Pro  
130 135 140  
Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly Gly Ser Gly  
145 150 155 160  
Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val Thr Glu Ala  
165 170 175  
Leu Val Ala Tyr Gly Val Ser Val Tyr  
180 185

<210> 627

<211> 198

<212> PRT

<213> Lysobacter enzymogenes

<400> 627

Ala Asn Ile Val Gly Gly Ile Glu Tyr Ser Ile Asn Asn Ala Ser Leu  
1 5 10 15  
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Ala Thr Lys Gly Phe Val  
20 25 30  
Thr Ala Gly His Cys Gly Thr Val Asn Ala Thr Ala Arg Ile Gly Gly  
35 40 45

Ala Val Val Gly Thr Phe Ala Ala Arg Val Phe Pro Gly Asn Asp Arg  
50 55 60  
Ala Trp Val Ser Leu Thr Ser Ala Gln Thr Leu Leu Pro Arg Val Ala  
65 70 75 80  
Asn Gly Ser Ser Phe Val Thr Val Arg Gly Ser Thr Glu Ala Ala Val  
85 90 95  
Gly Ala Ala Val Cys Arg Ser Gly Arg Thr Thr Gly Tyr Gln Cys Gly  
100 105 110  
Thr Ile Thr Ala Lys Asn Val Thr Ala Asn Tyr Ala Glu Gly Ala Val  
115 120 125  
Arg Gly Leu Thr Gln Gly Asn Ala Cys Met Gly Arg Gly Asp Ser Gly  
130 135 140  
Gly Ser Trp Ile Thr Ser Ala Gly Gln Ala Gln Gly Val Met Ser Gly  
145 150 155 160  
Gly Asn Val Gln Ser Asn Gly Asn Asn Cys Gly Ile Pro Ala Ser Gln  
165 170 175  
Arg Ser Ser Leu Phe Glu Arg Leu Gln Pro Ile Leu Ser Gln Tyr Gly  
180 185 190  
Leu Ser Leu Val Thr Gly  
195

<210> 628

<211> 191

<212> PRT

<213> Streptomyces fradiae

<400> 628

Ile Ala Gly Gly Glu Ala Ile Tyr Ala Ala Gly Gly Gly Arg Cys Ser  
1 5 10 15  
Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Ala Thr Tyr Ala Leu Thr  
20 25 30  
Ala Gly His Cys Thr Glu Ile Ala Ser Thr Trp Tyr Thr Asn Ser Gly  
35 40 45  
Gln Thr Ser Leu Leu Gly Thr Arg Ala Gly Thr Ser Phe Pro Gly Asn  
50 55 60  
Asp Tyr Gly Leu Ile Arg His Ser Asn Ala Ser Ala Ala Asp Gly Arg  
65 70 75 80  
Val Tyr Leu Tyr Asn Gly Ser Tyr Arg Asp Ile Thr Gly Ala Gly Asn  
85 90 95  
Ala Tyr Val Gly Gln Thr Val Gln Arg Ser Gly Ser Thr Thr Gly Leu  
100 105 110  
His Ser Gly Arg Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly  
115 120 125  
Gly Asp Ile Val Ser Gly Leu Ile Gln Thr Asn Val Cys Ala Glu Pro  
130 135 140  
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Ser Thr Ala Leu Gly Leu  
145 150 155 160  
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe  
165 170 175  
Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Ile Leu  
180 185 190

<210> 629

<211> 181

<212> PRT

<213> Streptomyces griseus

<400> 629

Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu  
1 5 10 15  
Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly  
20 25 30  
His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly  
35 40 45  
Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His Ser Asn Pro  
50 55 60  
Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp  
65 70 75 80  
Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser  
85 90 95  
Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala  
100 105 110  
Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr  
115 120 125  
Asn Val Cys Ala Gln Pro Gly Asp Ser Gly Gly Ser Leu Phe Ala Gly  
130 135 140  
Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr  
145 150 155 160  
Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr  
165 170 175  
Gly Ala Thr Val Leu  
180

<210> 630

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 630

Pro Arg Thr Met Phe Asp  
1 5

<210> 631

<211> 10

<212> PRT

<213> Cellulomonas strain 69B4

<400> 631

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr  
1 5 10

<210> 632

<211> 9

<212> PRT

<213> Cellulomonas strain 69B4

<400> 632

Thr Ala Asn Pro Thr Gly Thr Phe Ala  
1 5

<210> 633  
<211> 12  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 633

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala  
1 5 10

<210> 634  
<211> 14  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 634

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val  
1 5 10

<210> 635  
<211> 10  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 635

Arg Thr Gly Ala Gly Val Asn Leu Leu Ala  
1 5 10

<210> 636  
<211> 9  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 636

Phe Phe Gln Pro Val Asn Pro Ile Leu  
1 5

<210> 637

<211> 11  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 637

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala  
1 5 10

<210> 638

<211> 13  
<212> PRT  
<213> Cellulomonas strain 69B4

<400> 638

<210> 639

<211> 255

<212> PRT

<213> Streptogrisin C

<400> 639

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg  
 1 5 10 15  
 Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala  
 20 25 30  
 Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Thr Asn Gly Val Asn  
 35 40 45  
 Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp  
 50 55 60  
 Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val  
 65 70 75 80  
 Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser  
 85 90 95  
 Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His  
 100 105 110  
 Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly  
 115 120 125  
 Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp  
 130 135 140  
 Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser  
 145 150 155 160  
 Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro  
 165 170 175  
 Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly  
 180 185 190  
 Gly Gly Thr Pro Thr Asp Pro Pro Thr Thr Pro Pro Thr Asp Ser Pro  
 195 200 205  
 Gly Gly Thr Trp Ala Val Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val  
 210 215 220  
 Thr Tyr Gly Gly Ala Thr Tyr Arg Cys Leu Gln Ala His Thr Ala Gln  
 225 230 235 240  
 Pro Gly Trp Thr Pro Ala Asp Val Pro Ala Leu Trp Gln Arg Val  
 245 250 255

<210> 640

<211> 185

<212> PRT

<213> Streptogrisin B

<400> 640

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu

1 5 10 15  
Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly

20 25 30  
His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser Ala Arg Thr  
35 40 45  
Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn Asn Asp Tyr  
50 55 60  
Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp Gly Thr Val  
65 70 75 80  
Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly Met Ala  
85 90 95  
Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly Ser Val Thr  
100 105 110  
Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Asp Val Val Tyr Gly  
115 120 125  
Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Pro  
130 135 140  
Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly Gly Ser Gly  
145 150 155 160  
Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val Thr Glu Ala  
165 170 175  
Leu Ser Ala Tyr Gly Val Ser Val Tyr  
180 185

<210> 641

<211> 181

<212> PRT

<213> Streptogrisin A

<400> 641

Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu  
1 5 10 15  
Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly  
20 25 30  
His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly  
35 40 45  
Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His Ser Asn Pro  
50 55 60  
Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp  
65 70 75 80  
Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser  
85 90 95  
Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala  
100 105 110  
Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr  
115 120 125  
Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Ser Leu Phe Ala Gly  
130 135 140  
Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr  
145 150 155 160  
Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr  
165 170 175  
Gly Ala Thr Val Leu  
180

<210> 642

<211> 188

<212> PRT

<213> Streptogrisin D

<400> 642

Ile Ala Gly Gly Asp Ala Ile Trp Gly Ser Gly Ser Arg Cys Ser Leu  
1 5 10 15  
Gly Phe Asn Val Val Lys Gly Gly Glu Pro Tyr Phe Leu Thr Ala Gly  
20 25 30  
His Cys Thr Glu Ser Val Thr Ser Trp Ser Asp Thr Gln Gly Gly Ser  
35 40 45  
Glu Ile Gly Ala Asn Glu Gly Ser Ser Phe Pro Glu Asn Asp Tyr Gly  
50 55 60  
Leu Val Lys Tyr Thr Ser Asp Thr Ala His Pro Ser Glu Val Asn Leu  
65 70 75 80  
Tyr Asp Gly Ser Thr Gln Ala Ile Thr Gln Ala Gly Asp Ala Thr Val  
85 90 95  
Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val His Asp Gly

100 105 110  
Glu Val Thr Ala Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly Asp Ile  
115 120 125  
Val Asn Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser  
130 135 140  
Gly Gly Ala Leu Phe Ala Gly Asp Thr Ala Leu Gly Leu Thr Ser Gly  
145 150 155 160  
Gly Ser Gly Asp Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val  
165 170 175  
Pro Glu Ala Leu Ala Ala Tyr Gly Ala Glu Ile Gly  
180 185

<210> 643

<211> 198

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<220>

<221> VARIANT

<222> (9)..(10)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (12)..(12)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (22)..(23)

<223> Xaa can be any naturally occurring amino acid

<220>  
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<220>  
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<222> (43)..(51)  
<223> Xaa can be any naturally occurring amino acid

<220>  
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<222> (55)..(56)  
<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT  
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<223> Xaa can be any naturally occurring amino acid

<220>  
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<223> Xaa can be any naturally occurring amino acid

<220>  
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<222> (84)..(84)  
<223> Xaa can be any naturally occurring amino acid

<220>  
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<223> Xaa can be any naturally occurring amino acid

<220>  
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<222> (89)..(89)  
<223> Xaa can be any naturally occurring amino acid

<220>  
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<222> (92)..(92)  
<223> Xaa can be any naturally occurring amino acid

<220>  
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<222> (95)..(95)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (97)..(97)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (100)..(100)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (103)..(103)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (111)..(111)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (113)..(113)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (127)..(127)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (129)..(129)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (132)..(132)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (155)..(155)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
<222> (179)..(179)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT

<222> (191)..(198)

<223> Xaa can be any naturally occurring amino acid

<400> 643

Ile Ala Gly Gly Asp Ala Ile Tyr Xaa Xaa Gly Xaa Ser Arg Cys Ser  
1 5 10 15  
Leu Gly Phe Asn Val Xaa Xaa Gly Xaa Xaa Xaa Tyr Phe Leu Thr Ala  
20 25 30  
Gly His Cys Thr Xaa Xaa Gly Thr Thr Trp Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45  
Xaa Xaa Xaa Ile Gly Thr Xaa Xaa Gly Ser Ser Phe Pro Xaa Asn Asp  
50 55 60  
Tyr Gly Ile Val Arg Tyr Thr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val  
65 70 75 80  
Asn Xaa Tyr Xaa Gly Xaa Xaa Gln Xaa Ile Thr Xaa Ala Gly Xaa Ala  
85 90 95  
Xaa Val Gly Xaa Ala Val Xaa Arg Ser Gly Ser Thr Thr Gly Xaa His  
100 105 110  
Xaa Gly Ser Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Xaa Gly  
115 120 125  
Xaa Ile Val Xaa Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly  
130 135 140  
Asp Ser Gly Gly Ser Leu Phe Ala Gly Ser Xaa Ala Leu Gly Leu Thr  
145 150 155 160  
Ser Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln  
165 170 175  
Pro Val Xaa Glu Ala Leu Ser Ala Tyr Gly Leu Thr Val Ile Xaa Xaa  
180 185 190  
Xaa Xaa Xaa Xaa Xaa  
195

<210> 644

<211> 513

<212> PRT

<213> Thermus aquaticus

<400> 644

Met Arg Lys Thr Tyr Trp Leu Met Ala Leu Phe Ala Val Leu Val Leu  
1 5 10 15  
Gly Gly Cys Gln Met Ala Ser Arg Ser Asp Pro Thr Pro Thr Leu Ala  
20 25 30  
Glu Ala Phe Trp Pro Lys Glu Ala Pro Val Tyr Gly Leu Asp Asp Pro  
35 40 45  
Glu Ala Ile Pro Gly Arg Tyr Ile Val Val Phe Lys Lys Gly Lys Gly  
50 55 60  
Gln Ser Leu Leu Gln Gly Gly Ile Thr Thr Leu Gln Ala Arg Leu Ala  
65 70 75 80  
Pro Gln Gly Val Val Val Thr Gln Ala Tyr Thr Gly Ala Leu Gln Gly  
85 90 95  
Phe Ala Ala Glu Met Ala Pro Gln Ala Leu Glu Ala Phe Arg Gln Ser  
100 105 110  
Pro Asp Val Glu Phe Ile Glu Ala Asp Lys Val Val Arg Ala Trp Ala  
115 120 125  
Thr Gln Ser Pro Ala Pro Trp Gly Leu Asp Arg Ile Asp Gln Arg Asp  
130 135 140

Leu Pro Leu Ser Asn Ser Tyr Thr Tyr Thr Ala Thr Gly Arg Gly Val  
 145 150 155 160  
 Asn Val Tyr Val Ile Asp Thr Gly Ile Arg Thr Thr His Arg Glu Phe  
 165 170 175  
 Gly Gly Arg Ala Arg Val Gly Tyr Asp Ala Leu Gly Gly Asn Gly Gln  
 180 185 190  
 Asp Cys Asn Gly His Gly Thr His Val Ala Gly Thr Ile Gly Gly Val  
 195 200 205  
 Thr Tyr Gly Val Ala Lys Ala Val Asn Leu Tyr Ala Val Arg Val Leu  
 210 215 220  
 Asp Cys Asn Gly Ser Gly Ser Thr Ser Gly Val Ile Ala Gly Val Asp  
 225 230 235 240  
 Trp Val Thr Arg Asn His Arg Arg Pro Ala Val Ala Asn Met Ser Leu  
 245 250 255  
 Gly Gly Gly Val Ser Thr Ala Leu Asp Asn Ala Val Lys Asn Ser Ile  
 260 265 270  
 Ala Ala Gly Val Val Tyr Ala Val Ala Ala Gly Asn Asp Asn Ala Asn  
 275 280 285  
 Ala Cys Asn Tyr Ser Pro Ala Arg Val Ala Glu Ala Leu Thr Val Gly  
 290 295 300  
 Ala Thr Thr Ser Ser Asp Ala Arg Ala Ser Phe Ser Asn Tyr Gly Ser  
 305 310 315 320  
 Cys Val Asp Leu Phe Ala Pro Gly Ala Ser Ile Pro Ser Ala Trp Tyr  
 325 330 335  
 Thr Ser Asp Thr Ala Thr Gln Thr Leu Asn Gly Thr Ser Met Ala Thr  
 340 345 350  
 Pro His Val Ala Gly Val Ala Ala Leu Tyr Leu Glu Gln Asn Pro Ser  
 355 360 365  
 Ala Thr Pro Ala Ser Val Ala Ser Ala Ile Leu Asn Gly Ala Thr Thr  
 370 375 380  
 Gly Arg Leu Ser Gly Ile Gly Ser Gly Ser Pro Asn Arg Leu Leu Tyr  
 385 390 395 400  
 Ser Leu Leu Ser Ser Gly Ser Gly Ser Thr Ala Pro Cys Thr Ser Cys  
 405 410 415  
 Ser Tyr Tyr Thr Gly Ser Leu Ser Gly Pro Gly Asp Tyr Asn Phe Gln  
 420 425 430  
 Pro Asn Gly Thr Tyr Tyr Ser Pro Ala Gly Thr His Arg Ala Trp  
 435 440 445  
 Leu Arg Gly Pro Ala Gly Thr Asp Phe Asp Leu Tyr Leu Trp Arg Trp  
 450 455 460  
 Asp Gly Ser Arg Trp Leu Thr Val Gly Ser Ser Thr Gly Pro Thr Ser  
 465 470 475 480  
 Glu Glu Ser Leu Ser Tyr Ser Gly Thr Ala Gly Tyr Tyr Leu Trp Arg  
 485 490 495  
 Ile Tyr Ala Tyr Ser Gly Ser Gly Met Tyr Glu Phe Trp Leu Gln Arg  
 500 505 510  
 Pro

<210> 645  
 <211> 495  
 <212> PRT  
 <213> Cellulomonas strain 69B4  
 <400> 645

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala

1 5 10 15  
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu Pro Ala  
20 25 30  
Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala Glu Lys Leu Asp  
35 40 45  
Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp Ala Glu  
50 55 60  
Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu Thr Gly  
65 70 75 80  
Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr Trp Val  
85 90 95  
Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala Val Glu  
100 105 110  
Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His Ser Leu  
115 120 125  
Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu Glu Gly  
130 135 140  
His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn Ser Val  
145 150 155 160  
Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly Leu Val  
165 170 175  
Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu Thr Asp  
180 185 190  
Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr  
195 200 205  
Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn Gly Gly  
210 215 220  
Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn  
225 230 235 240  
Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala  
245 250 255  
Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val Asn Asn  
260 265 270  
Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala Pro Val  
275 280 285  
Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly  
290 295 300  
Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly Thr Val  
305 310 315 320  
Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly  
325 330 335  
Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly  
340 345 350  
Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Asn  
355 360 365  
Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr Thr Asp Ser Gly  
370 375 380  
Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly Tyr Ala Arg Thr  
385 390 395 400  
Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala Gln Pro Asn Gly  
405 410 415  
Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser Val Cys Leu Asn  
420 425 430  
Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln Arg Trp Asn Gly  
435 440 445  
Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro Gly Ser Asn Glu  
450 455 460

Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg Tyr Val Val Asn  
465 470 475 480  
Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu Thr Leu Pro  
485 490 495

<210> 646  
<211> 510  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> consensus sequence

<220>  
<221> VARIANT  
<222> (3)...(509)  
<223> Xaa can be any naturally occurring amino acid

<400> 646

Met Ala Xaa Xaa Ala Xaa Xaa Leu Leu Ala Gly Xaa Xaa Xaa Ala Xaa  
1 5 10 15  
Xaa Xaa Asp Pro Xaa Pro Xaa Xaa Ala Xaa Ala Xaa Xaa Pro Lys Xaa  
20 25 30  
Ala Xaa Xaa Xaa Xaa Asp Xaa Xaa Glu Ala Ile Xaa Xaa Xaa Xaa  
35 40 45  
Xaa Leu Xaa Xaa Xaa Xaa Ala Xaa Ala Xaa Xaa Xaa Gln Xaa Xaa  
50 55 60  
Xaa Xaa Xaa Xaa Xaa Xaa Leu Ala Xaa Xaa Xaa Xaa Leu Xaa  
65 70 75 80  
Xaa Xaa Phe Xaa Gly Xaa  
85 90 95  
Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Asp Xaa Glu Xaa Xaa Xaa  
100 105 110  
Ala Xaa Xaa Val Xaa Xaa Ala Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa  
115 120 125  
Xaa Leu Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Tyr  
130 135 140  
Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Val Xaa Xaa Ile Xaa Xaa  
145 150 155 160  
Gly Xaa Ala Xaa Val Xaa  
165 170 175  
Xaa Asp Ala Leu Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa  
180 185 190  
Xaa Met Xaa Xaa Ile Gly Gly Xaa Xaa Tyr Xaa Ile Ala Xaa Xaa  
195 200 205  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Ala  
210 215 220  
Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa  
225 230 235 240  
Xaa Xaa Ala Xaa Xaa Xaa Xaa Ser Xaa Ala Gly Xaa Xaa Xaa Xaa Ala  
245 250 255  
Xaa Asp Xaa Ala Xaa Xaa Xaa Ser Xaa Ala Ala Xaa Xaa Xaa Xaa Xaa  
260 265 270  
Xaa Xaa Xaa Xaa Asn Xaa Xaa Ala Asn Xaa Xaa Asn Tyr Ser Xaa Ala  
275 280 285  
Arg Val Xaa Xaa Ala Xaa Xaa Ala Ala Xaa Xaa Ser Xaa Xaa

290	295	300
Xaa Xaa Ser Xaa Ser Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
305	310	315
Xaa Ala Xaa Xaa Xaa Ser Xaa Xaa Tyr Xaa Xaa Xaa Thr Xaa Xaa Xaa		
325	330	335
Xaa Ile Xaa Xaa Thr Xaa Xaa Ala Xaa Pro Xaa Xaa Ala Gly Xaa Ala		
340	345	350
Xaa Leu Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Thr Xaa Ala Xaa Xaa Ala		
355	360	365
Xaa Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
370	375	380
Xaa Xaa Ala Xaa Xaa Xaa Leu Xaa Ser Xaa Xaa Ser Xaa Gly Ser		
385	390	395
Xaa Xaa Xaa Xaa Xaa Thr Ser Cys Ser Xaa Tyr Xaa Xaa Ser Xaa		
405	410	415
Ser Gly Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Gln Pro Asn Gly Ser		
420	425	430
Tyr Xaa Xaa Xaa Xaa Xaa Ala Gly Thr His Xaa Xaa Xaa Leu Xaa Gly		
435	440	445
Pro Ala Gly Xaa Asp Phe Asp Leu Tyr Leu Xaa Arg Trp Xaa Gly Ser		
450	455	460
Xaa Trp Leu Thr Val Ala Xaa Ser Thr Xaa Pro Xaa Ser Xaa Glu Ser		
465	470	475
Ile Ser Tyr Xaa Gly Xaa Ala Gly Tyr Tyr Xaa Trp Xaa Ile Xaa Ala		
485	490	495
Xaa Ser Gly Ser Gly Xaa Tyr Xaa Xaa Xaa Leu Xaa Xaa Pro		
500	505	510

<210> 647

<211> 190

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<220>

<221> VARIANT

<222> (6)..(188)

<223> Xaa can be any naturally occurring amino acid

<400> 647

Asp Val Ile Gly Gly Xaa Xaa Tyr Xaa Ile Xaa Xaa Xaa Xaa Arg Xaa		
1	5	10
Xaa Xaa Xaa Xaa Cys Ser Ile Gly Phe Ala Val Xaa Gly Gly Phe Val		
20	25	30
Thr Ala Gly His Cys Gly Arg Xaa Gly Ala Xaa Xaa Xaa Xaa Xaa Xaa		
35	40	45
Thr Ser Xaa Pro Xaa Gly Thr Phe Xaa Gly Ser Ser Phe Pro Gly Asn		
50	55	60
Asp Tyr Ala Trp Val Gln Val Ala Ser Gly Asn Thr Pro Val Gly Ala		
65	70	75
Val Asn Asn Tyr Ser Gly Gly Thr Val Xaa Val Ala Gly Ser Thr Xaa		
85	90	95
Ala Ala Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp		
100	105	110

<210> 648  
<211> 368  
<212> PRT  
<213> *Theunekifida fuscata*

<100> 648

Met	Asn	His	Ser	Ser	Arg	Arg	Thr	Thr	Ser	Leu	Leu	Phe	Thr	Ala	Ala
1					5				10				15		
Leu	Ala	Ala	Thr	Ala	Leu	Val	Ala	Ala	Thr	Thr	Pro	Ala	Ser	Ala	Gln
					20				25				30		
Glu	Leu	Ala	Leu	Lys	Arg	Asp	Leu	Gly	Leu	Ser	Asp	Ala	Glu	Val	Ala
					35				40				45		
Glu	Leu	Arg	Ala	Ala	Glu	Ala	Glu	Ala	Val	Glu	Leu	Glu	Glu	Leu	
					50				55			60			
Arg	Asp	Ser	Leu	Gly	Ser	Asp	Phe	Gly	Gly	Val	Tyr	Leu	Asp	Ala	Asp
65					70					75				80	
Thr	Thr	Glu	Ile	Thr	Val	Ala	Val	Thr	Asp	Pro	Ala	Ala	Val	Ser	Arg
					85				90				95		
Val	Asp	Ala	Asp	Asp	Val	Thr	Val	Asp	Val	Val	Asp	Phe	Gly	Glu	Thr
					100				105				110		
Ala	Leu	Asn	Asp	Phe	Val	Ala	Ser	Leu	Asn	Ala	Ile	Ala	Asp	Thr	Ala
					115				120				125		
Asp	Pro	Lys	Val	Thr	Gly	Trp	Tyr	Thr	Asp	Leu	Glu	Ser	Asp	Ala	Val
					130				135			140			
Val	Ile	Thr	Thr	Leu	Arg	Gly	Gly	Thr	Pro	Ala	Ala	Glu	Glu	Leu	Ala
145					150				155				160		
Glu	Arg	Ala	Gly	Leu	Asp	Glu	Arg	Ala	Val	Arg	Ile	Val	Glu	Glu	Asp
					165				170				175		
Glu	Glu	Pro	Gln	Ser	Leu	Ala	Ala	Ile	Ile	Gly	Gly	Asn	Pro	Tyr	Tyr
					180				185				190		
Phe	Gly	Asn	Tyr	Arg	Cys	Ser	Ile	Gly	Phe	Ser	Val	Arg	Gln	Gly	Ser
					195				200				205		
Gln	Thr	Gly	Phe	Ala	Thr	Ala	Gly	His	Cys	Gly	Ser	Thr	Gly	Thr	Arg
					210				215			220			
Val	Ser	Ser	Pro	Ser	Gly	Thr	Val	Ala	Gly	Ser	Tyr	Phe	Pro	Gly	Arg
225					230				235				240		
Asp	Met	Gly	Trp	Val	Arg	Ile	Thr	Ser	Ala	Asp	Thr	Val	Thr	Pro	Leu
					245				250				255		
Val	Asn	Arg	Tyr	Asn	Gly	Gly	Thr	Val	Thr	Val	Thr	Gly	Ser	Gln	Glu
					260				265				270		
Ala	Ala	Thr	Gly	Ser	Ser	Val	Cys	Arg	Ser	Gly	Ala	Thr	Thr	Gly	Trp
					275				280				285		
Arg	Cys	Gly	Thr	Ile	Gln	Ser	Lys	Asn	Gln	Thr	Val	Arg	Tyr	Ala	Glu
					290				295			300			
Gly	Thr	Val	Thr	Gly	Leu	Thr	Arg	Thr	Thr	Ala	Cys	Ala	Glu	Gly	Gly

305	310	315	320
Asp Ser Gly Gly Pro Trp Leu Thr Gly Ser Gln Ala Gln Gly Val Thr			
325	330	335	
Ser Gly Gly Thr Gly Asp Cys Arg Ser Gly Gly Ile Thr Phe Phe Gln			
340	345	350	
Pro Ile Asn Pro Leu Leu Ser Tyr Phe Gly Leu Gln Leu Val Thr Gly			
355	360	365	

<210> 649  
<211> 382  
<212> PRT  
<213> Streptomyces spp.

<400> 649

Met Arg His Thr Gly Arg Asn Ala Ile Gly Ala Ala Ile Ala Ala Ser			
1	5	10	15
Ala Leu Ala Phe Ala Leu Val Pro Ser Gln Ala Ala Asn Asp Thr			
20	25	30	
Leu Thr Glu Arg Ala Glu Ala Ala Val Ala Asp Leu Pro Ala Gly Val			
35	40	45	
Leu Asp Ala Met Glu Arg Asp Leu Gly Leu Ser Glu Gln Glu Ala Gly			
50	55	60	
Leu Lys Leu Val Ala Glu His Asp Ala Ala Leu Leu Gly Glu Thr Leu			
65	70	75	80
Ser Ala Asp Leu Asp Ala Phe Ala Gly Ser Trp Leu Ala Glu Gly Thr			
85	90	95	
Glu Leu Val Val Ala Thr Thr Ser Glu Ala Glu Ala Glu Ile Thr			
100	105	110	
Glu Ala Gly Ala Thr Ala Glu Val Val Asp His Thr Leu Ala Glu Leu			
115	120	125	
Asp Ser Val Lys Asp Ala Leu Asp Thr Ala Ala Glu Ser Tyr Asp Thr			
130	135	140	
Thr Asp Ala Pro Val Trp Tyr Val Asp Val Thr Thr Asn Gly Val Val			
145	150	155	160
Leu Leu Thr Ser Asp Val Thr Glu Ala Glu Gly Phe Val Glu Ala Ala			
165	170	175	
Gly Val Asn Ala Ala Ala Val Asp Ile Gln Thr Ser Asp Glu Gln Pro			
180	185	190	
Gln Ala Phe Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Met Gly Gly			
195	200	205	
Gly Arg Cys Ser Val Gly Phe Ser Val Thr Gln Gly Ser Thr Pro Gly			
210	215	220	
Phe Ala Thr Ala Gly His Cys Gly Thr Val Gly Thr Ser Thr Thr Gly			
225	230	235	240
Tyr Asn Gln Ala Ala Gln Gly Thr Phe Glu Glu Ser Ser Phe Pro Gly			
245	250	255	
Asp Asp Met Ala Trp Val Ser Val Asn Ser Asp Trp Asn Thr Thr Pro			
260	265	270	
Thr Val Asn Glu Gly Glu Val Thr Val Ser Gly Ser Thr Glu Ala Ala			
275	280	285	
Val Gly Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys			
290	295	300	
Gly Thr Ile Gln Gln His Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr			
305	310	315	320
Ile Thr Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser			
325	330	335	

Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly  
340 345 350  
Gly Ser Gly Asn Cys Thr Ser Gly Gly Thr Thr Tyr His Gln Pro Ile  
355 360 365  
Asn Pro Leu Leu Ser Ala Tyr Gly Leu Asp Leu Val Thr Gly  
370 375 380

<210> 650  
<211> 388  
<212> PRT  
<213> Streptomyces spp.

<400> 650

Met Arg Leu Lys Gly Arg Thr Val Ala Ile Gly Ser Ala Leu Ala Ala  
1 5 10 15  
Ser Ala Leu Ala Leu Ser Leu Val Pro Ala Asn Ala Ser Ser Glu Leu  
20 25 30  
Pro Ser Ala Glu Thr Ala Lys Ala Asp Ala Leu Val Glu Gln Leu Pro  
35 40 45  
Ala Gly Met Val Asp Ala Met Glu Arg Asp Leu Gly Val Pro Ala Ala  
50 55 60  
Glu Val Gly Asn Gln Leu Val Ala Glu His Glu Ala Ala Val Leu Glu  
65 70 75 80  
Glu Ser Leu Ser Glu Asp Leu Ser Gly Tyr Ala Gly Ser Trp Ile Val  
85 90 95  
Glu Gly Thr Ser Glu His Val Val Ala Thr Thr Asp Arg Ala Glu Ala  
100 105 110  
Ala Glu Ile Thr Ala Ala Gly Ala Thr Ala Thr Val Val Glu His Ser  
115 120 125  
Leu Ala Glu Leu Glu Ala Val Lys Asp Ile Leu Asp Glu Ala Ala Thr  
130 135 140  
Ala Asn Pro Glu Asp Ala Ala Pro Val Trp Tyr Val Asp Val Thr Thr  
145 150 155 160  
Asn Glu Val Val Val Leu Ala Ser Asp Val Pro Ala Ala Glu Ala Phe  
165 170 175  
Val Ala Ala Ser Gly Ala Asp Ala Ser Thr Val Arg Val Glu Arg Ser  
180 185 190  
Asp Glu Ser Pro Gln Pro Phe Tyr Asp Leu Val Gly Gly Asp Ala Tyr  
195 200 205  
Tyr Ile Gly Asn Gly Arg Cys Ser Ile Gly Phe Ser Val Arg Gln Gly  
210 215 220  
Ser Thr Pro Gly Phe Val Thr Ala Gly His Cys Gly Ser Val Gly Asn  
225 230 235 240  
Ala Thr Thr Gly Phe Asn Arg Val Ser Gln Gly Thr Phe Arg Gly Ser  
245 250 255  
Trp Phe Pro Gly Arg Asp Met Ala Trp Val Ala Val Asn Ser Asn Trp  
260 265 270  
Thr Pro Thr Ser Leu Val Arg Asn Ser Gly Ser Gly Val Arg Val Thr  
275 280 285  
Gly Ser Thr Gln Ala Thr Val Gly Ser Ser Ile Cys Arg Ser Gly Ser  
290 295 300  
Thr Thr Gly Trp Arg Cys Gly Thr Ile Gln Gln His Asn Thr Ser Val  
305 310 315 320  
Thr Tyr Pro Gln Gly Thr Ile Thr Gly Val Thr Arg Thr Ser Ala Cys  
325 330 335  
Ala Gln Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly Thr Gln Ala

340                    345                    350  
Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ile Gly Gly Thr  
355                    360                    365  
Thr Phe His Gln Pro Val Asn Pro Ile Leu Ser Gln Tyr Gly Leu Thr  
370                    375                    380  
Leu Val Arg Ser  
385

<210> 651  
<211> 458  
<212> PRT  
<213> Streptomyces lividans  
  
<400> 651

Met Val Gly Arg His Ala Ala Arg Ser Arg Arg Ala Ala Leu Thr Ala  
1                    5                    10                    15  
Leu Gly Ala Leu Val Leu Thr Ala Leu Pro Ser Ala Ala Ser Ala Ala  
20                    25                    30  
Pro Pro Pro Val Pro Gly Pro Arg Pro Ala Val Ala Arg Thr Pro Asp  
35                    40                    45  
Ala Ala Thr Ala Pro Ala Arg Met Leu Ser Ala Met Glu Arg Asp Leu  
50                    55                    60  
Arg Leu Ala Pro Gly Gln Ala Ala Ala Arg Pro Val Asn Glu Ala Glu  
65                    70                    75                    80  
Ala Gly Thr Arg Ala Gly Met Leu Arg Asn Thr Leu Gly Asp Arg Phe  
85                    90                    95  
Ala Gly Ala Trp Val Ser Gly Ala Thr Ser Ala Glu Leu Thr Val Ala  
100                    105                    110  
Thr Thr Asp Ala Ala Asp Thr Ala Ala Ile Glu Ala Gln Gly Ala Lys  
115                    120                    125  
Ala Ala Val Val Gly Arg Asn Leu Ala Glu Leu Arg Ala Val Lys Glu  
130                    135                    140  
Lys Leu Asp Ala Ala Ala Val Arg Thr Arg Thr Arg Gln Thr Pro Val  
145                    150                    155                    160  
Trp Tyr Val Asp Val Lys Thr Asn Arg Val Thr Val Gln Ala Thr Gly  
165                    170                    175  
Ala Ser Ala Ala Ala Ala Phe Val Glu Ala Ala Gly Val Pro Ala Ala  
180                    185                    190  
Asp Val Gly Val Arg Val Ser Pro Asp Gln Pro Arg Val Leu Glu Asp  
195                    200                    205  
Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg Cys Ser  
210                    215                    220  
Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala Thr Ala  
225                    230                    235                    240  
Gly His Cys Gly Asp Pro Gly Ala Thr Thr Gly Tyr Asn Glu Ala  
245                    250                    255  
Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp Met Ala  
260                    265                    270  
Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Lys Ala  
275                    280                    285  
Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala Leu Val  
290                    295                    300  
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly  
305                    310                    315                    320  
Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly Thr Val  
325                    330                    335

Asp Gly Leu Thr Gly Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly  
340 345 350  
Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser Gly Gly  
355 360 365  
Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro Val Asn  
370 375 380  
Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser Ala Ala  
385 390 395 400  
Thr Gln Thr Pro Ala Pro Gln Asp Asn Ala Ala Ala Asp Ala Trp Thr  
405 410 415  
Ala Gly Arg Val Tyr Glu Val Gly Thr Thr Val Ser Tyr Asp Gly Val  
420 425 430  
Arg Tyr Arg Cys Leu Gln Ser His Gln Ala Gln Gly Val Gly Ser Pro  
435 440 445  
Ala Ser Val Pro Ala Leu Trp Gln Arg Val  
450 455

<210> 652

<211> 458

<212> PRT

<213> Streptomyces coelicolor A3(2)

<400> 652

Met Val Gly Arg His Ala Ala Arg Ser Arg Arg Ala Ala Leu Thr Ala  
1 5 10 15  
Leu Gly Ala Leu Val Leu Thr Ala Leu Pro Ser Ala Ala Ser Ala Ala  
20 25 30  
Pro Pro Pro Val Pro Gly Pro Arg Pro Ala Val Ala Arg Thr Pro Asp  
35 40 45  
Ala Ala Thr Ala Pro Ala Arg Met Leu Ser Ala Met Glu Arg Asp Leu  
50 55 60  
Arg Leu Ala Pro Gly Gln Ala Ala Ala Arg Leu Val Asn Glu Ala Glu  
65 70 75 80  
Ala Gly Thr Arg Ala Gly Met Leu Arg Asn Thr Leu Gly Asp Arg Phe  
85 90 95  
Ala Gly Ala Trp Val Ser Gly Ala Thr Ser Ala Glu Leu Thr Val Ala  
100 105 110  
Thr Thr Asp Ala Ala Asp Thr Ala Ala Ile Glu Ala Gln Gly Ala Lys  
115 120 125  
Ala Ala Val Val Gly Arg Asn Leu Ala Glu Leu Arg Ala Val Lys Glu  
130 135 140  
Lys Leu Asp Ala Ala Ala Val Arg Thr Arg Thr Arg Gln Thr Pro Val  
145 150 155 160  
Trp Tyr Val Asp Val Lys Thr Asn Arg Val Thr Val Gln Ala Thr Gly  
165 170 175  
Ala Ser Ala Ala Ala Ala Phe Val Glu Ala Ala Gly Val Pro Ala Ala  
180 185 190  
Asp Val Gly Val Arg Val Ser Pro Asp Gln Pro Arg Val Leu Glu Asp  
195 200 205  
Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg Cys Ser  
210 215 220  
Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala Thr Ala  
225 230 235 240  
Gly His Cys Gly Asp Pro Gly Ala Thr Thr Gly Tyr Asn Glu Ala  
245 250 255  
Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp Met Ala

260	265	270
Trp Val Gly Val Asn Ser Asp	Trp Thr Ala Thr Pro Asp	Val Lys Ala
275	280	285
Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val	Glu Ala Leu Val	
290	295	300
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr	Thr Gly Trp His Cys Gly	
305	310	315
320		
Thr Ile Gln Gln His Asp Thr Ser Val	Thr Tyr Pro Glu Gly	Thr Val
325	330	335
Asp Gly Leu Thr Glu Thr Thr Val	Cys Ala Glu Pro Gly	Asp Ser Gly
340	345	350
Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly	Thr Thr Ser Gly Gly	
355	360	365
Ser Gly Asp Cys Thr Asn Gly Gly	Thr Phe Tyr Gln Pro Val Asn	
370	375	380
Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys	Thr Thr Ser Ala Ala	
385	390	395
400		
Thr Gln Thr Pro Ala Pro Gln Asp Asn Ala Ala	Asp Ala Trp Thr	
405	410	415
Ala Gly Arg Val Tyr Glu Val Gly	Thr Thr Val Ser Tyr Asp Gly	Val
420	425	430
Arg Tyr Arg Cys Leu Gln Ser His Gln Ala Gln Gly	Val Gly Ser Pro	
435	440	445
Ala Ser Val Pro Ala Leu Trp Gln Arg Val		
450	455	

<210> 653

<211> 456

<212> PRT

<213> Streptomyces avermitilis MA-4680

<400> 653

Met Val His Arg His Val Gly Ala Gly Cys Ala Gly Leu Ser Val Leu

1	5	10	15
Ala Thr Leu Val Leu Thr Gly Leu Pro	Ala Ala Ala Ala Ile	Glu Pro	
20	25	30	
Pro Gly Pro Ala Pro Ala Pro Ser	Ala Val Gln Pro Leu Gly	Ala Gly	
35	40	45	
Asn Pro Ser Thr Ala Val Leu Gly	Ala Leu Gln Arg Asp	Leu His Leu	
50	55	60	
Thr Asp Thr Gln Ala Lys	Thr Arg Leu Val Asn	Glu Met Glu Ala Gly	
65	70	75	80
Thr Arg Ala Gly Arg Leu Gln Asn	Ala Leu Gly Lys His	Phe Ala Gly	
85	90	95	
Ala Trp Val His Gly Ala Ala Ser	Ala Asp Leu Thr Val	Ala Thr Thr	
100	105	110	
His Ala Thr Asp Ile Pro Ala Ile	Thr Ala Gly Gly	Ala Thr Ala Val	
115	120	125	
Val Val Lys Thr Gly Leu Asp Asp	Leu Lys Gly Ala Lys	Lys Lys Leu	
130	135	140	
Asp Ser Ala Val Ala His Gly Gly	Thr Ala Val Asn	Thr Pro Val Arg	
145	150	155	160
Tyr Val Asp Val Arg Thr Asn Arg Val	Thr Leu Gln Ala Arg	Ser Arg	
165	170	175	

Ala Ala Ala Asp Ala Leu Ile Ala Ala Gly Val Asp Ser Gly Leu  
                  180             185             190  
 Val Asp Val Lys Val Ser Glu Asp Arg Pro Arg Ala Leu Phe Asp Ile  
                  195             200             205  
 Arg Gly Gly Asp Ala Tyr Tyr Ile Asp Asn Thr Ala Arg Cys Ser Val  
                  210             215             220  
 Gly Phe Ser Val Thr Lys Gly Asn Gln Gln Gly Phe Ala Thr Ala Gly  
                  225             230             235             240  
 His Cys Gly Arg Ala Gly Ala Pro Thr Ala Gly Phe Asn Glu Val Ala  
                  245             250             255  
 Gln Gly Thr Val Gln Ala Ser Val Phe Pro Gly His Asp Met Ala Trp  
                  260             265             270  
 Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Ala Gly Ala  
                  275             280             285  
 Ala Gly Gln Asn Val Ser Ile Ala Gly Ser Val Gln Ala Ile Val Gly  
                  290             295             300  
 Ala Ala Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr  
                  305             310             315             320  
 Val Glu Glu His Asp Thr Ser Val Thr Tyr Glu Glu Gly Thr Val Asp  
                  325             330             335  
 Gly Leu Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly  
                  340             345             350  
 Ser Phe Val Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser  
                  355             360             365  
 Gly Asp Cys Thr Arg Gly Gly Thr Thr Tyr Tyr Gln Pro Val Asn Pro  
                  370             375             380  
 Ile Leu Ser Thr Tyr Gly Leu Thr Leu Lys Thr Ser Thr Ala Pro Thr  
                  385             390             395             400  
 Asp Thr Pro Ser Asp Pro Val Asp Gln Ser Gly Val Trp Ala Ala Gly  
                  405             410             415  
 Arg Val Tyr Glu Val Gly Ala Gln Val Thr Tyr Ala Gly Val Thr Tyr  
                  420             425             430  
 Gln Cys Leu Gln Ser His Gln Ala Gln Gly Val Trp Gln Pro Ala Ala  
                  435             440             445  
 Thr Pro Ala Leu Trp Gln Arg Leu  
                  450             455

<210> 654  
 <211> 458  
 <212> PRT  
 <213> Streptomyces lividans

<400> 654

Met Pro His Arg His Arg His Arg Ala Val Gly Ala Ala Val Ala  
                  1             5             10             15  
 Ala Thr Ala Ala Leu Leu Val Ala Gly Leu Ser Gly Ser Ala Ser Ala  
                  20             25             30  
 Gly Thr Ala Pro Ala Gly Ser Ala Pro Thr Ala Ala Glu Thr Leu Arg  
                  35             40             45  
 Thr Asp Ala Ala Pro Pro Ala Leu Leu Lys Ala Met Gln Arg Asp Leu  
                  50             55             60  
 Gly Ile Asp Arg Arg Gln Ala Glu Arg Arg Leu Val Asn Glu Ala Glu  
                  65             70             75             80  
 Ala Gly Ala Thr Ala Gly Arg Leu Arg Ala Ala Leu Gly Gly Asp Phe  
                  85             90             95  
 Ala Gly Ala Trp Val Arg Gly Ala Glu Ser Gly Thr Leu Thr Val Ala

	100	105	110
Thr	Thr Asp Ala Gly Asp Val	Ala Ala Val Glu Ala Arg Gly Ala Glu	
	115	120	125
Ala	Lys Val Val Arg His Ser Leu Ala Asp Leu Asp Ala Ala Lys Ala		
	130	135	140
Arg	Leu Asp Thr Ala Ala Gly Leu Asn Thr Ala Asp Ala Pro Val		
	145	150	155
Trp	Tyr Val Asp Thr Arg Thr Asn Thr Val Val Val Glu Ala Ile Arg		
	165	170	175
Pro	Ala Ala Ala Arg Ser Leu Leu Thr Ala Ala Gly Val Asp Gly Ser		
	180	185	190
Leu	Ala His Val Lys Asn Arg Thr Glu Arg Pro Arg Thr Phe Tyr Asp		
	195	200	205
Leu	Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg Cys Ser		
	210	215	220
Ile	Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala Thr Ala		
	225	230	235
Gly	His Cys Asp Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn Arg Val		
	245	250	255
Ala	Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp Met Ala		
	260	265	270
Trp	Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val Leu Gly		
	275	280	285
Ala	Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser Pro Val		
	290	295	300
Gly	Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly		
	305	310	315
Thr	Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly Thr Ile		
	325	330	335
Ser	Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly		
	340	345	350
Gly	Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly		
	355	360	365
Ser	Gly Asp Cys Arg Thr Gly Gly Gly Thr Phe Phe Gln Pro Ile Asn		
	370	375	380
Ala	Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly Gly Asp		
	385	390	395
Asp	Gly Gly Gly Asp Asp Gly Gly Glu Glu Pro Gly Gly Thr Trp Ala		
	405	410	415
Ala	Gly Thr Val Tyr Gln Pro Gly Asp Thr Val Thr Tyr Gly Gly Ala		
	420	425	430
Thr	Phe Arg Cys Leu Gln Gly His Gln Ala Tyr Ala Gly Trp Glu Pro		
	435	440	445
Pro	Asn Val Pro Ala Leu Trp Gln Arg Val		
	450	455	

<210> 655

<211> 463

<212> PRT

<213> Streptomyces coelicolor A3 (2)

<400> 655

Met	Pro His Arg His Arg His His Arg Ala Val Gly Ala Ala Val Ala		
1	5	10	15
Ala	Thr Ala Ala Leu Leu Val Ala Gly Leu Ser Gly Ser Ala Ser Ala		
	20	25	30

Gly Thr Ala Pro Ala Gly Ser Ala Pro Thr Ala Ala Glu Thr Leu Arg  
     35                        40                        45  
 Thr Asp Ala Ala Pro Pro Ala Leu Leu Lys Ala Met Gln Arg Asp Leu  
     50                        55                        60  
 Gly Leu Asp Arg Arg Gln Ala Glu Arg Arg Leu Val Asn Glu Ala Glu  
     65                        70                        75                        80  
 Ala Gly Ala Thr Ala Gly Arg Leu Arg Ala Ala Leu Gly Gly Asp Phe  
     85                        90                        95  
 Ala Gly Ala Trp Val Arg Gly Ala Glu Ser Gly Thr Leu Thr Val Ala  
     100                       105                       110  
 Thr Thr Asp Ala Gly Asp Val Ala Ala Ile Glu Ala Arg Gly Ala Glu  
     115                       120                       125  
 Ala Lys Val Val Arg His Ser Leu Ala Asp Leu Asp Ala Ala Lys Ala  
     130                       135                       140  
 Arg Leu Asp Thr Ala Ala Ala Gly Leu Asn Thr Ala Asp Ala Pro Val  
     145                       150                       155                       160  
 Trp Tyr Val Asp Thr Arg Thr Asn Thr Val Val Val Glu Ala Ile Arg  
     165                       170                       175  
 Pro Ala Ala Ala Arg Ser Leu Leu Thr Ala Ala Gly Val Asp Gly Ser  
     180                       185                       190  
 Leu Ala His Val Lys Asn Arg Thr Glu Arg Pro Arg Thr Phe Tyr Asp  
     195                       200                       205  
 Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg Cys Ser  
     210                       215                       220  
 Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala Thr Ala  
     225                       230                       235                       240  
 Gly His Cys Gly Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn Arg Val  
     245                       250                       255  
 Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp Met Ala  
     260                       265                       270  
 Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val Leu Gly  
     275                       280                       285  
 Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser Pro Val  
     290                       295                       300  
 Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly  
     305                       310                       315                       320  
 Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly Thr Ile  
     325                       330                       335  
 Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly  
     340                       345                       350  
 Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly  
     355                       360                       365  
 Ser Gly Asp Cys Arg Thr Gly Gly Glu Thr Phe Phe Gln Pro Ile Asn  
     370                       375                       380  
 Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly Gly Asp  
     385                       390                       395                       400  
 Asp Gly Gly Asp Asp Gly Gly Asp Asp Gly Gly Glu Glu Pro  
     405                       410                       415  
 Gly Gly Thr Trp Ala Ala Gly Thr Val Tyr Gln Pro Gly Asp Thr Val  
     420                       425                       430  
 Thr Tyr Gly Gly Ala Thr Phe Arg Cys Leu Gln Gly His Gln Ala Tyr  
     435                       440                       445  
 Ala Gly Trp Glu Pro Pro Asn Val Pro Ala Leu Trp Gln Arg Val  
     450                       455                       460

<210> 656  
 <211> 457

<212> PRT

<213> Streptomyces griseus

<400> 656

Met Glu Arg Thr Thr Leu Arg Arg Arg Ala Leu Val Ala Gly Thr Ala  
1 5 10 15  
Thr Val Ala Val Gly Ala Leu Ala Leu Ala Gly Leu Thr Gly Val Ala  
20 25 30  
Ser Ala Asp Pro Ala Ala Thr Ala Ala Pro Pro Val Ser Ala Asp Ser  
35 40 45  
Leu Ser Pro Gly Met Leu Ala Ala Leu Glu Arg Asp Leu Gly Leu Asp  
50 55 60  
Glu Asp Ala Ala Arg Ser Arg Ile Ala Asn Glu Tyr Arg Ala Ala Ala  
65 70 75 80  
Val Ala Ala Gly Leu Glu Lys Ser Leu Gly Ala Arg Tyr Ala Gly Ala  
85 90 95  
Arg Val Ser Gly Ala Lys Ala Thr Leu Thr Val Ala Thr Thr Asp Ala  
100 105 110  
Ser Glu Ala Ala Arg Ile Thr Glu Ala Gly Ala Arg Ala Glu Val Val  
115 120 125  
Gly His Ser Leu Asp Arg Phe Glu Gly Val Lys Lys Ser Leu Asp Lys  
130 135 140  
Ala Ala Leu Asp Lys Ala Pro Lys Asn Val Pro Val Trp Tyr Val Asp  
145 150 155 160  
Val Ala Ala Asn Arg Val Val Val Asn Ala Ala Ser Pro Ala Ala Gly  
165 170 175  
Gln Ala Phe Leu Lys Val Ala Gly Val Asp Arg Gly Leu Val Thr Val  
180 185 190  
Ala Arg Ser Ala Glu Gln Pro Arg Ala Leu Ala Asp Ile Arg Gly Gly  
195 200 205  
Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg Cys Ser Val Gly Phe Ser  
210 215 220  
Val Thr Arg Gly Thr Gln Asn Gly Phe Ala Thr Ala Gly His Cys Gly  
225 230 235 240  
Arg Val Gly Thr Thr Asn Gly Val Asn Gln Gln Ala Gln Gly Thr  
245 250 255  
Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp Ile Ala Trp Val Ala Thr  
260 265 270  
Asn Ala Asn Trp Thr Pro Arg Pro Leu Val Asn Gly Tyr Gly Arg Gly  
275 280 285  
Asp Val Thr Val Ala Gly Ser Thr Ala Ser Val Val Gly Ala Ser Val  
290 295 300  
Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Gln  
305 310 315 320  
Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr Ile Ser Gly Val Thr  
325 330 335  
Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile  
340 345 350  
Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys  
355 360 365  
Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro Ile Asn Pro Leu Leu Gln  
370 375 380  
Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly Gly Gly Thr Pro Thr Asp  
385 390 395 400  
Pro Pro Thr Thr Pro Pro Thr Asp Ser Pro Gly Gly Thr Trp Ala Val  
405 410 415

Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val Thr Tyr Gly Gly Ala Thr  
420 425 430  
Tyr Arg Cys Leu Gln Ala His Thr Ala Gln Pro Gly Trp Thr Pro Ala  
435 440 445  
Asp Val Pro Ala Leu Trp Gln Arg Val  
450 455